

Fig. 1.0

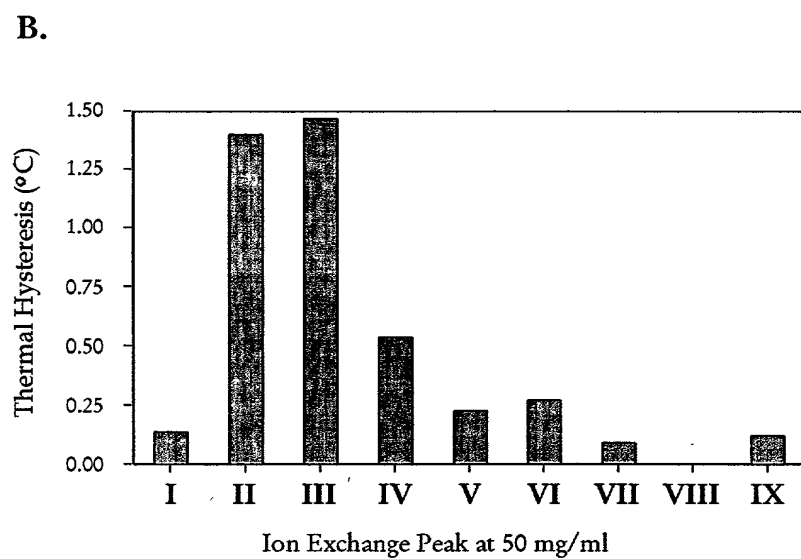
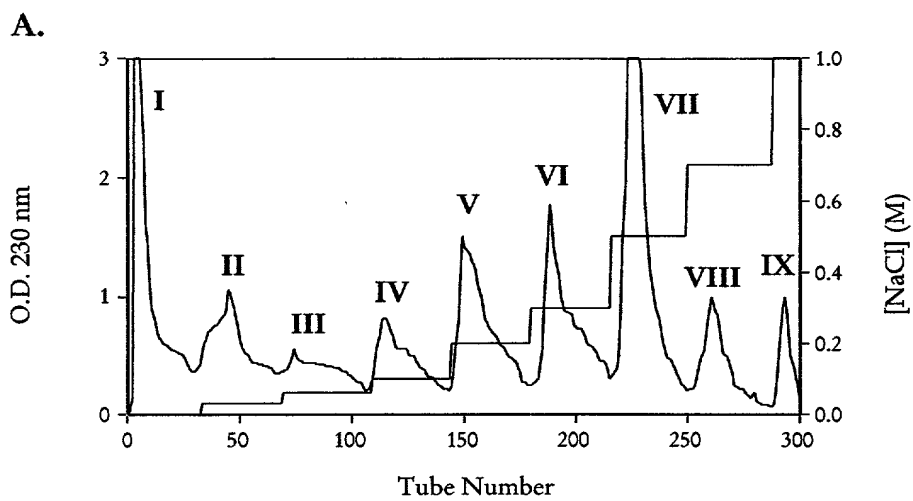


Fig. 1.1

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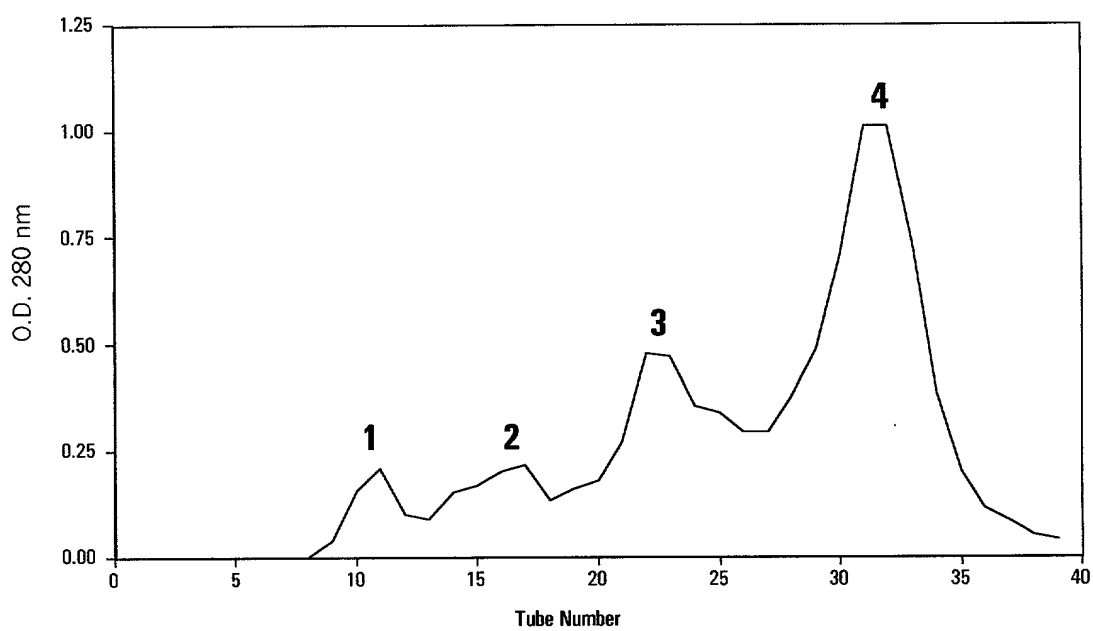


Fig. 1.2

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Fig. 1.3

Fig. 1.4

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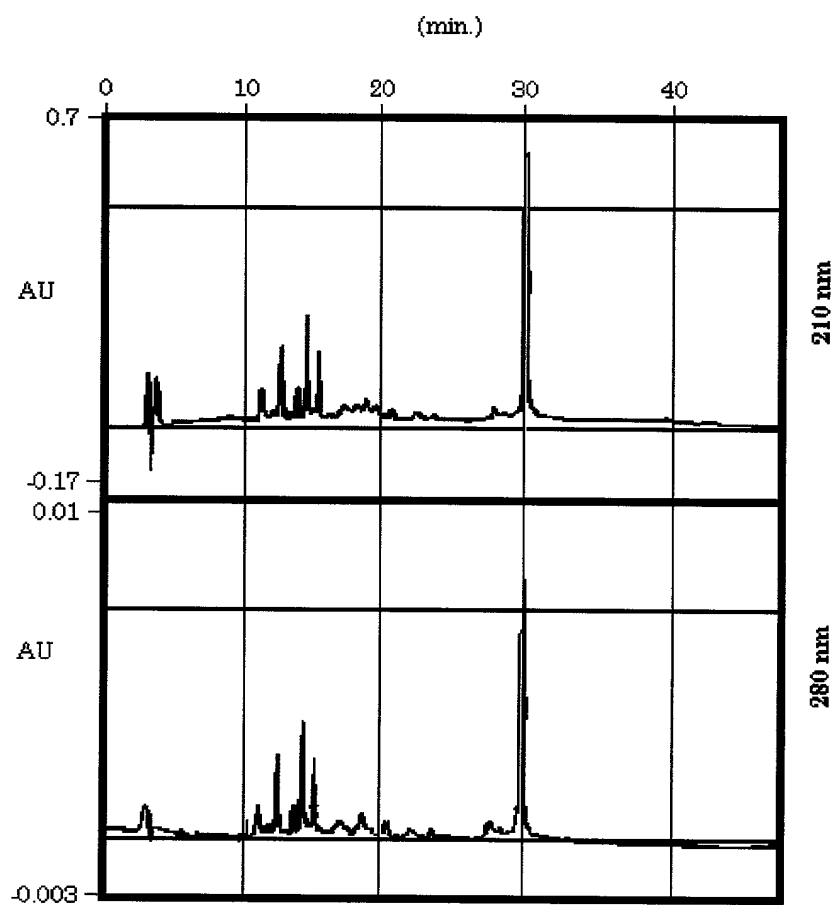


Fig. 1.5

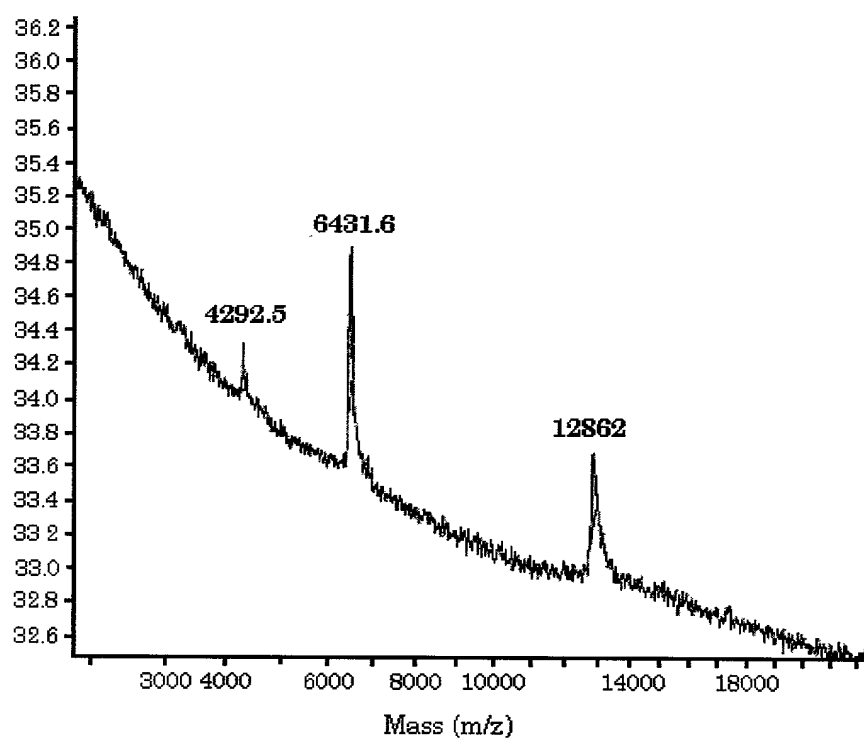


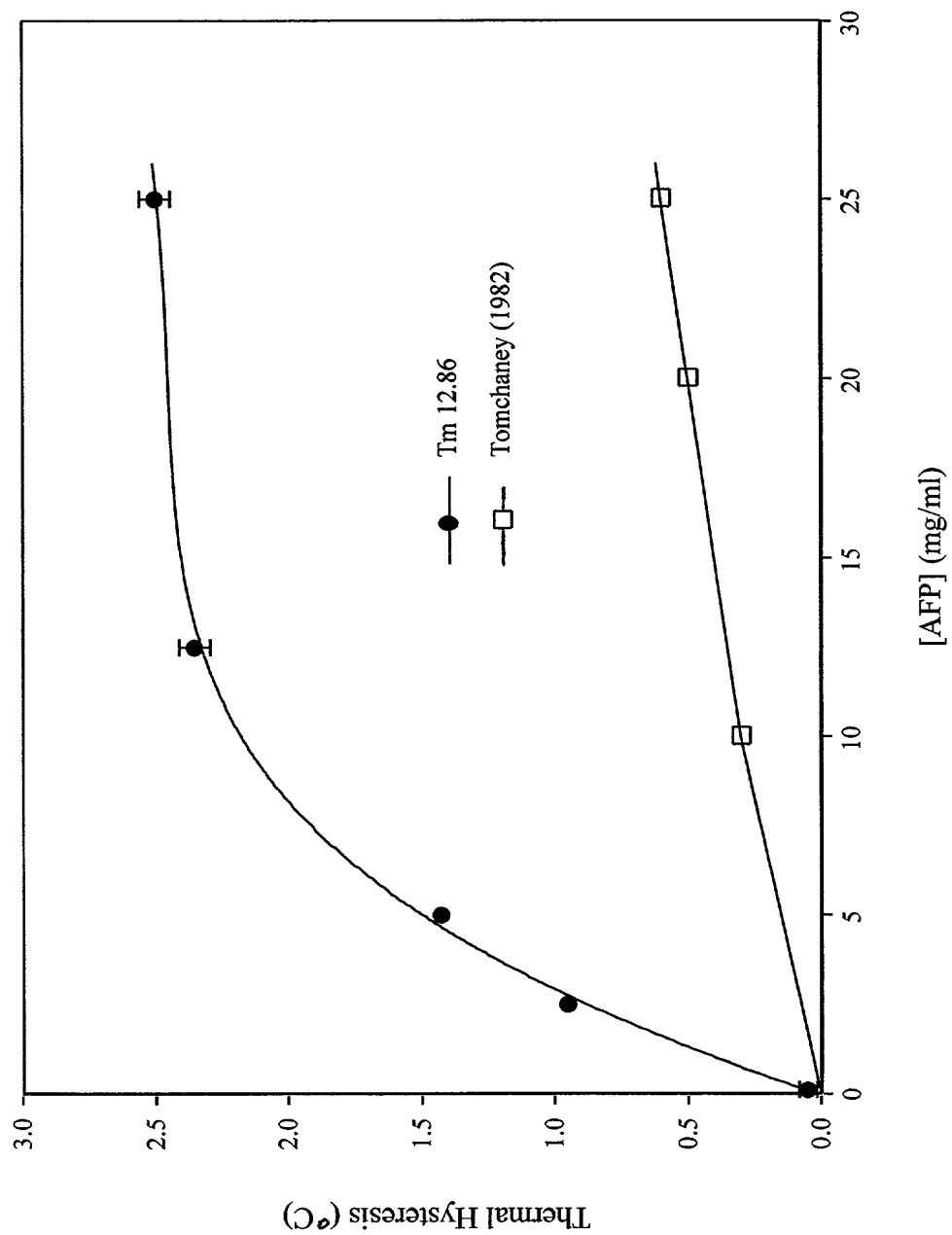
Fig. 1.6

Fig. 1.7

09070796.001.002

NH₂-L-T-D-E-Q-I-Q-K-R-N-K-I-S-K-E-?-Q-Q-V
Val Gln Gln Glu Lys Ser Ile Lys Asn Arg Lys Gln Ile Gln Asp Thr Leu

Fig. 1.8

*Fig. 1.9*

1 2.5 5 10 15 20 H

7.5

Fig. 1.10

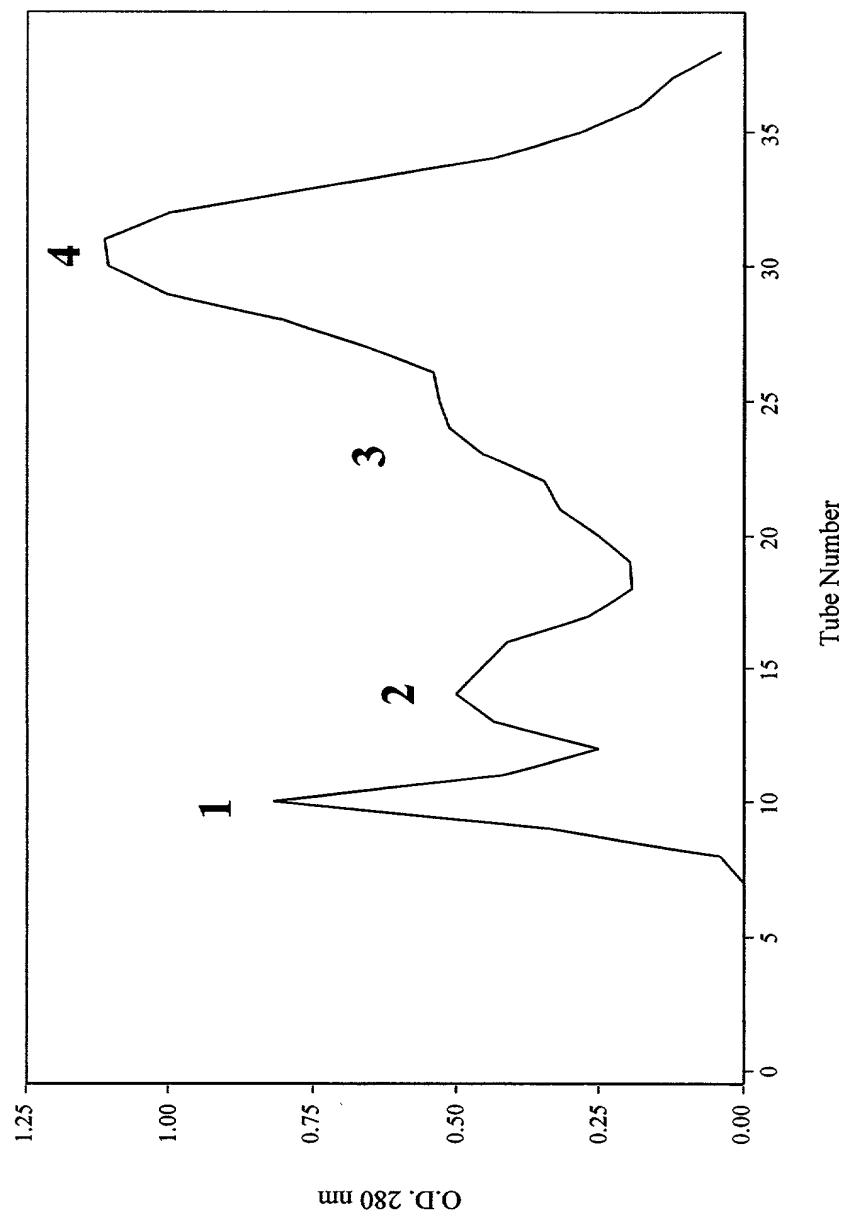


Fig. 1.11

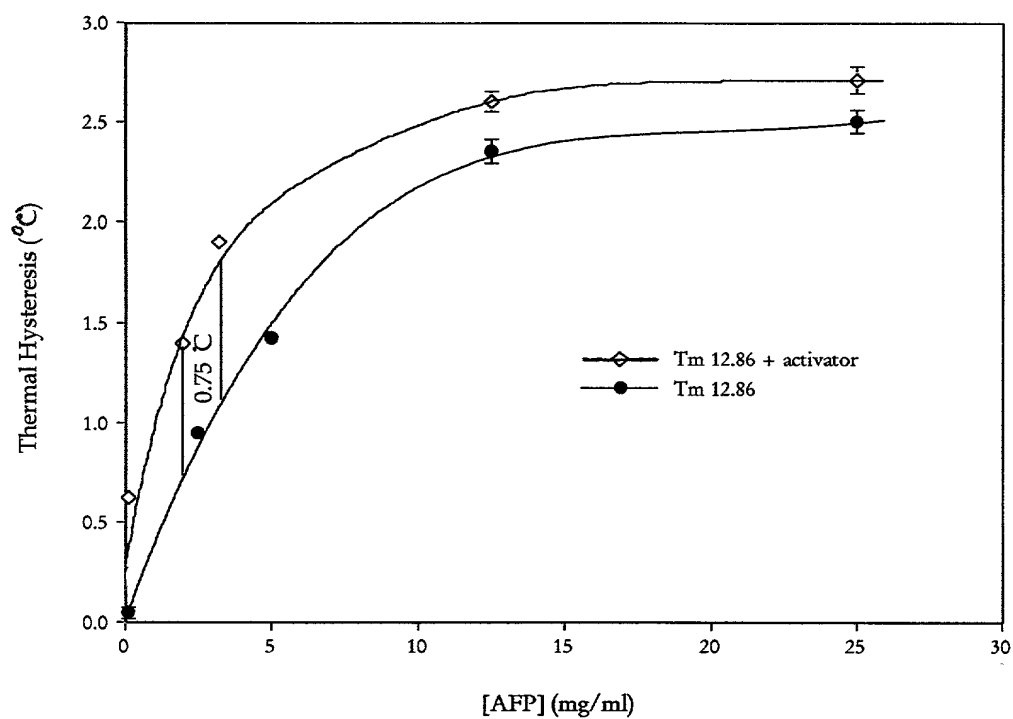
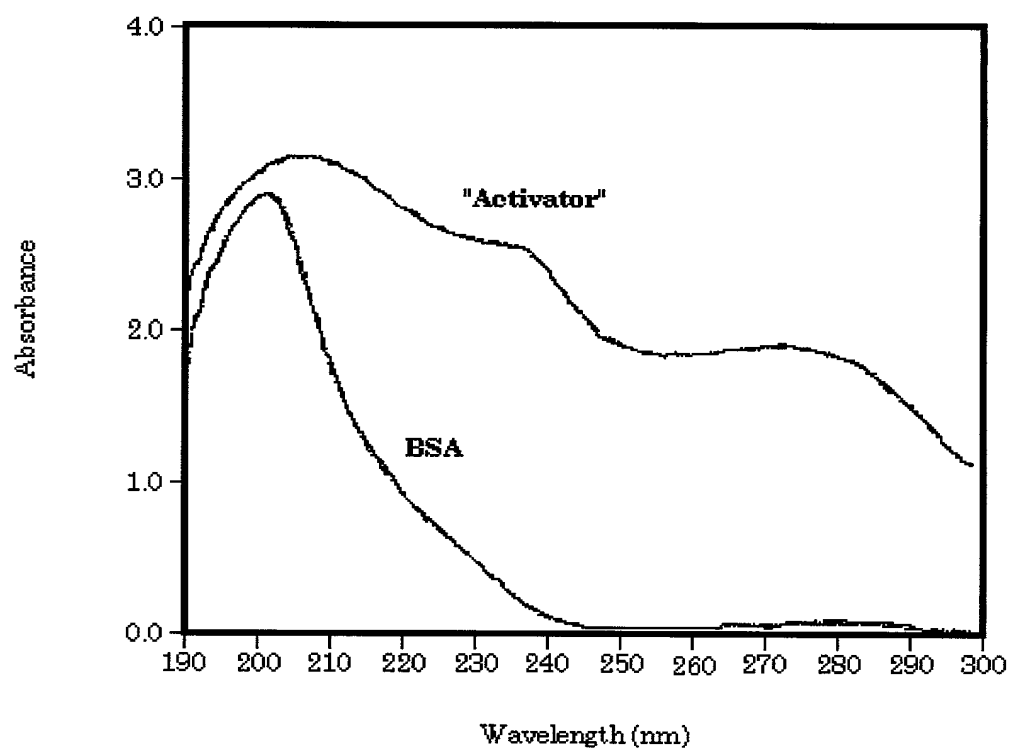


Fig. 1.12

*Fig. 1.13*

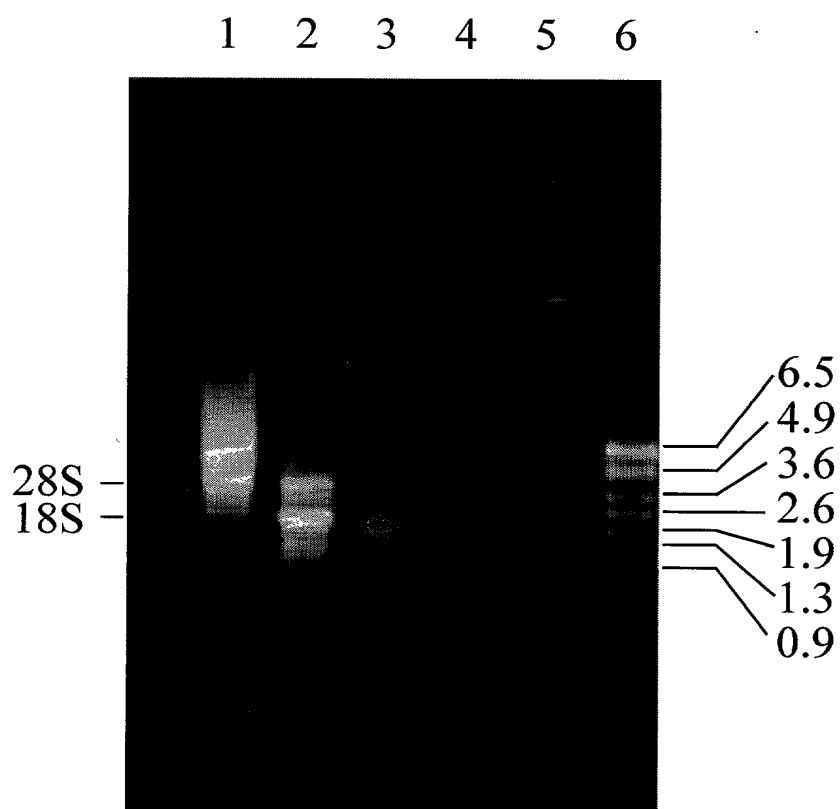


Fig. 2.0

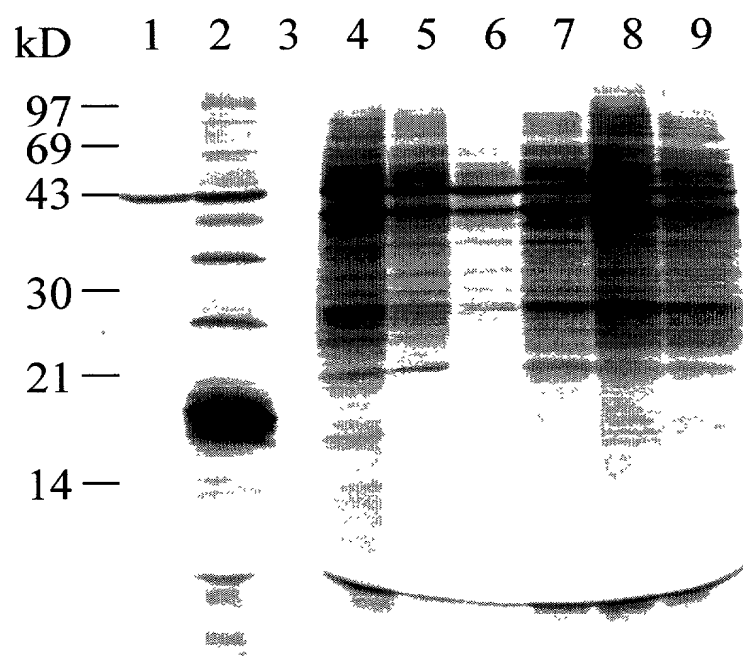


Fig. 2.1

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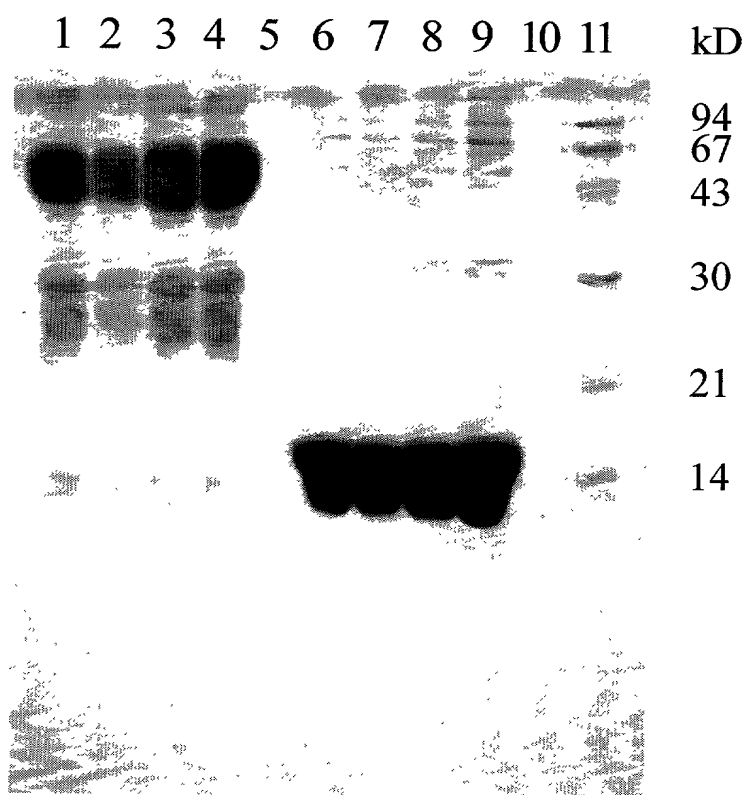


Fig. 2.2

1 2 3 4 5 6 7 8 9 kD

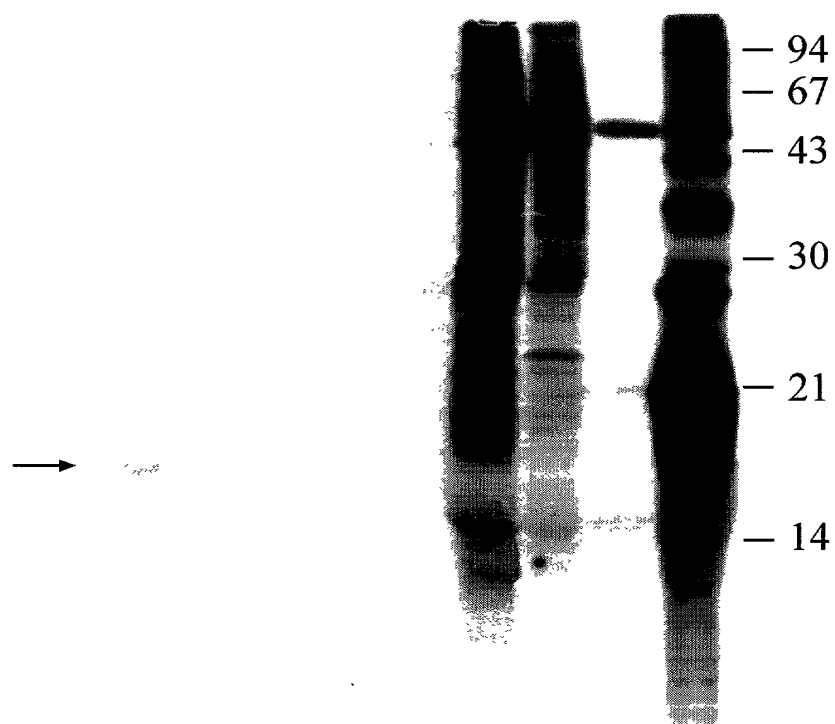


Fig. 2.3

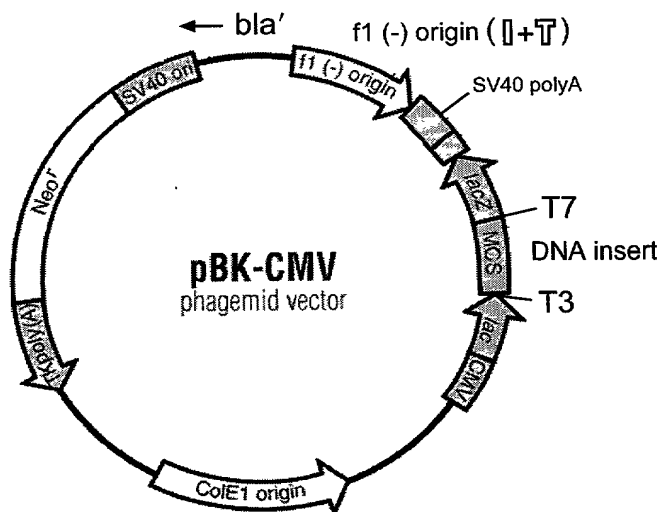
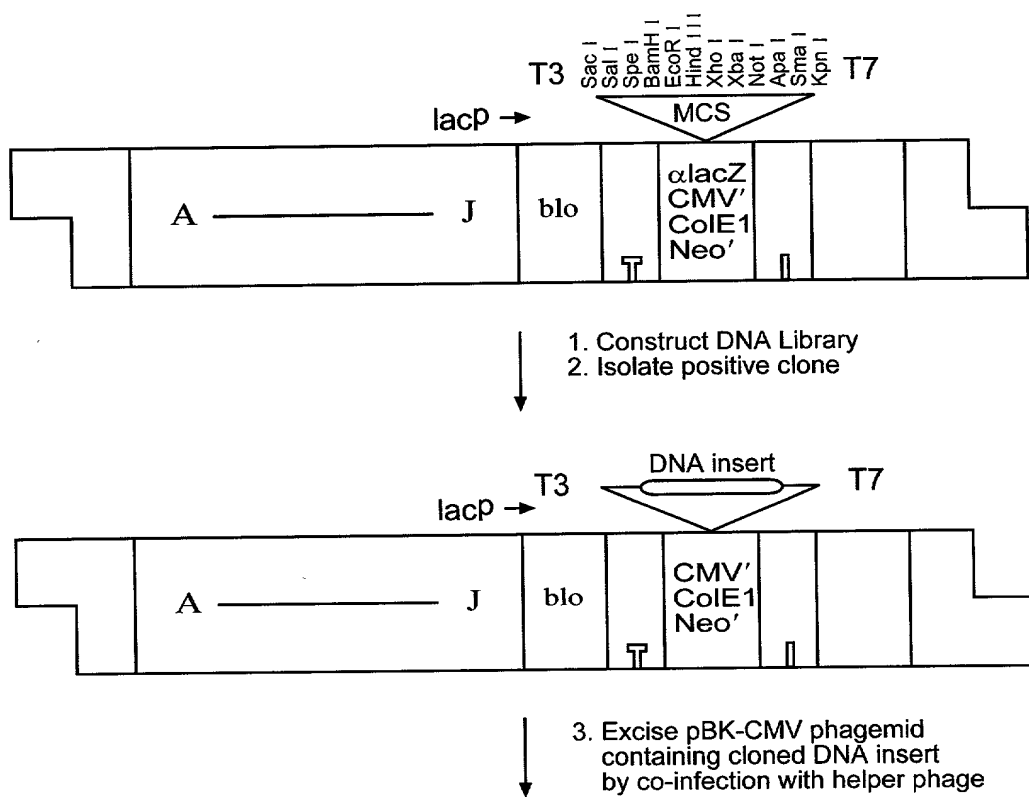
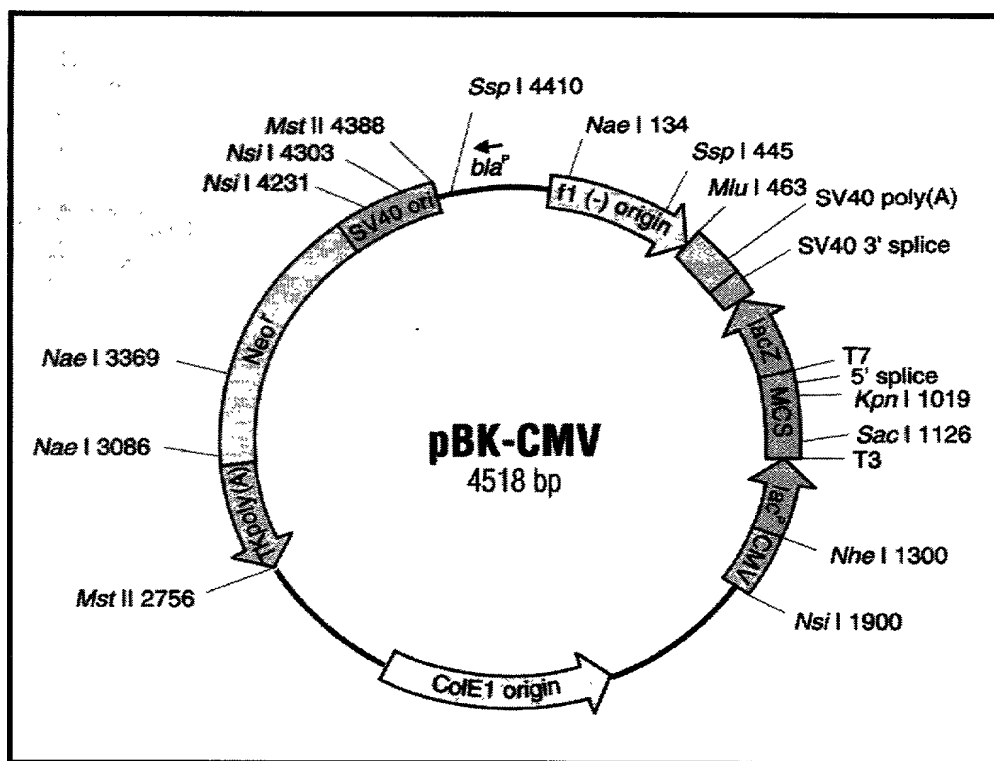


Fig. 2.4a

2025-09-29 09:29:29



BK Reverse Primer
 5' ACAGGAACAGCTATGACCTG 3'
 1200 MET
 5' TCACACAGGAAACAGCTATGACCTGATTACGCCAAGCTEGAAATTAACCTCACTAAAGGGAACAAAGCTGGAGCTCGCCGCTGCAGGTGACACTAGTGGATCCAAAG
 3' AGTGTGCTCTTTGTCTBATACTGSACTAATGCGSTTCGACCTTAAATGGGAATGATTTCCTTGTTCGACCTCGAGCGCGGAGCTCCAGCTGTGATCACTAGGTTCTTAA
 1183
 β-Galactosidase →
 Xho I
 Nhe I III Sca I Xba I Not I Ape I Cfa I Asp106 I BstX I Sma I Kpn I
 AATCAAAAAGCTTCTCGAGAGTACTTCTAGAGCGGCGCGGCGCCATCGATTTCCACCGGGTGGGGTACCAGGTAAAGTGTACCAATTCGCCCTATAGTGAATCTATTACAAATCACTGGCCGTGTTTTACA 3' (+)
 GTTTTCGAAGAGCTCTCATGAAGATCTCGCGGCGCCGCGGTAGCTAAAGGTGGGCCACCCCATGTTCCATTACATGGTTAAGCGGATATCACTACGATATAATGTTAAGTGACCGGAGCAAAATGT 5' (-)
 ← +1 T7 promoter 851
 3' CGGATATCACTCAGCATAATG 5' 3' TGACCGGCGCAAAATG 5'
 T7 Primer M13-20 Primer

Fig 2.4b

Agarose gel electrophoresis image showing six lanes. Lane 1: DNA ladder with bands at 2.3, 9.4, 6.6, 4.3, 2.0, and 0.56 kb. Lanes 2-5: Experimental samples showing various banding patterns. Lane 6: Another DNA ladder with bands at 2.3, 9.4, 6.6, 4.3, 2.0, and 0.56 kb.

Fig. 2.5

[illegible]

1 AGTGGATCCAAAGAATTCGGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTGCGTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAATAAAGTGTCTTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCCGCGGGCCCATCGTTTTCCACCC

X
h
o
I

X
b
o
I

Fig. 2.6a

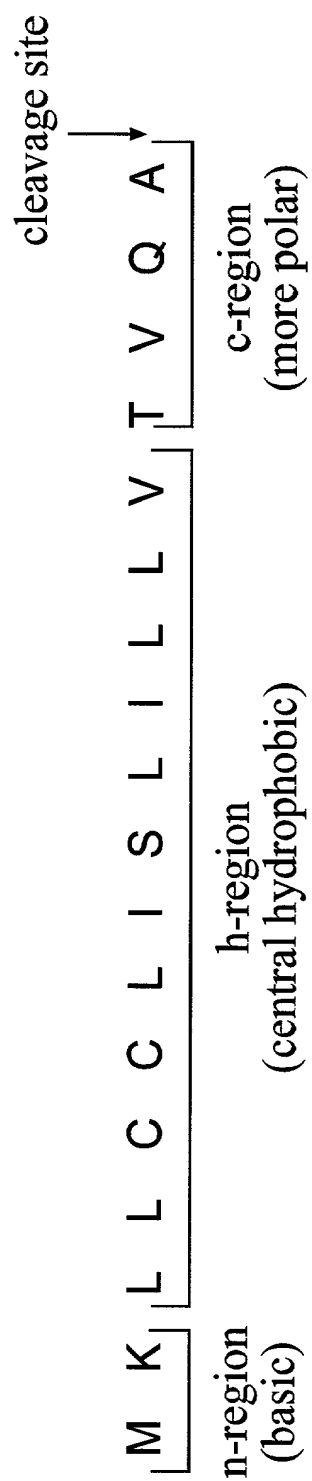


Fig. 2.6b

A. Mature Tm 13.17 amino acid residue

1 LTEAQIEKLN KISKKCQNES GVSQEIIITKA RNGDWEDDPK LKRQVFCVAR
 51 NAGLATESGE VVVDVLREKV RKVTDNDEET EKIINKCAVK RDTVEETVFN
 101 TFKCVMKNKP KFSPVD

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

<u>Residue</u>	<u>Number</u>	<u>Mole Percent</u>
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = Glu	13	11.207
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K = Lys	16	13.793
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V = Val	14	12.069
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

Fig. 2.6c

20210909 09:29:00

1	AOTGATCCAAAGAAATTCGGCACGAGACTACTAAGATGAA	Tm 13.17 B 1
41 1	GTTGCTCTGTTTCTCTATCTCTCTCATTTCTGTTGTTCAACA CTTACTTCTCTCATTTCTGTTGTTCAACA	Tm 13.17 B 1
81 28	GTTCAAGGCCCTGACCGAAGCACAATAATGAGAACTGAAACA GTTCAAGGCCATAACTTCAGGAAGGCCATGAGCTACTGCCCA	Tm 13.17 B 1
121 68	AGATCAGCAAAARAAATGTCRAARATGAAAGTGGAGTGTCTGCA AAACCAAGCGCAAGATGCAAGACATGAAAGTGGAGTGTCTGCA	Tm 13.17 B 1
161 118	AAGAATCATTAACCAARAGCTCCCAACGATGACTGGGAGGAC AAGCATCATTAAGAGAGCTCCCAAGAGATGACTTGGAGGAC	Tm 13.17 B 1
201 148	BATCCTTAARCTGAAACCGCAAGTTTCTTTGCGTGGCCCAAGGA DACCCTTAARCTGAAATGCAACTTCTTTGCAATTTTTCAGAGG	Tm 13.17 B 1
241 188	ACGCCTGCTCTGACCAAGGAATCGGAGAGAGTGGTGGTTCGA CACTCGAAGATAGTCCGGAATCGGAGAGAAATTTGAGGCGCA	Tm 13.17 B 1
281 228	CGTGTGAGAGGAGGAGAGTGAAGGAAGGTCACTGACCAACGAC CACGTTCAAGGAGGAGAGTTGACGAAGGTGACCAACGATGAT	Tm 13.17 B 1
321 268	GAGGAAACTGAGGAATATCATCAATTAAGTGCCTGCTCAAGA GAGGAAAAGCGAGGAAGATTTCTGAGAGTGCACGGTGACTG	Tm 13.17 B 1
361 308	GAGATACTGTTGAGGAGACGGTGTTCATATCTTTCAAAATG AACRCACCTCCGGAAGATACGCCAATTTGAGATTAACCAATG	Tm 13.17 B 1
401 348	TGTCATGAAAARCAAGCCCAAGTTCTCACCAAGTTGAATTGA TOTATGAAAGGACCAAGCCCAATTTCTTTTC	Tm 13.17 B 1
441 388	ACCAACCACGACTAGTAGATGTTTCAAAATGATGTTGCTTTAC AGACATATTGTTCTGAAAAGCTTTGT	Tm 13.17 B 1
481 428	ATATTAARAAATAAAGTGTCTTCTGATGTAAAAA GCACCA	Tm 13.17 B 1

Fig. 2.7

Tm 13.17	3	EAQIEKLNKISKKCQNESGVSEIITKARNGDWEDDPKLKRQVFCVARNA	52
		.. } } : :. . : :. : :.	
AFP-3	1	ETPREKLKQHSACKAESGVSEESLNKVRNREEVDDPKLKEHAFKILKRA	50
Tm 13.17	53	GLATESGEVVVDVLREKVRKVTNDDEETEKIINKCAVKRDTVEETVFNTF	102
		: .. . : :.. ... :... : ... :	
AFP-3	51	GFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPQHSSADFF	100
Tm 13.17	103	KCVMKNKP	110
		. :-	
AFP-3	101	KCVHDNRS	108

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

Fig. 2.8

Tm 13.17	M	K	L	L	C	C	L	I	S	L	I	L	V	T	V	Q	A
AFP-3	M	K	L	L	L	C	L	V	L	V	A	L	V	A	T	Y	A
B Protein				L	T	S	L	I	L	L	V	A	V	Q	A		

Fig. 2.9

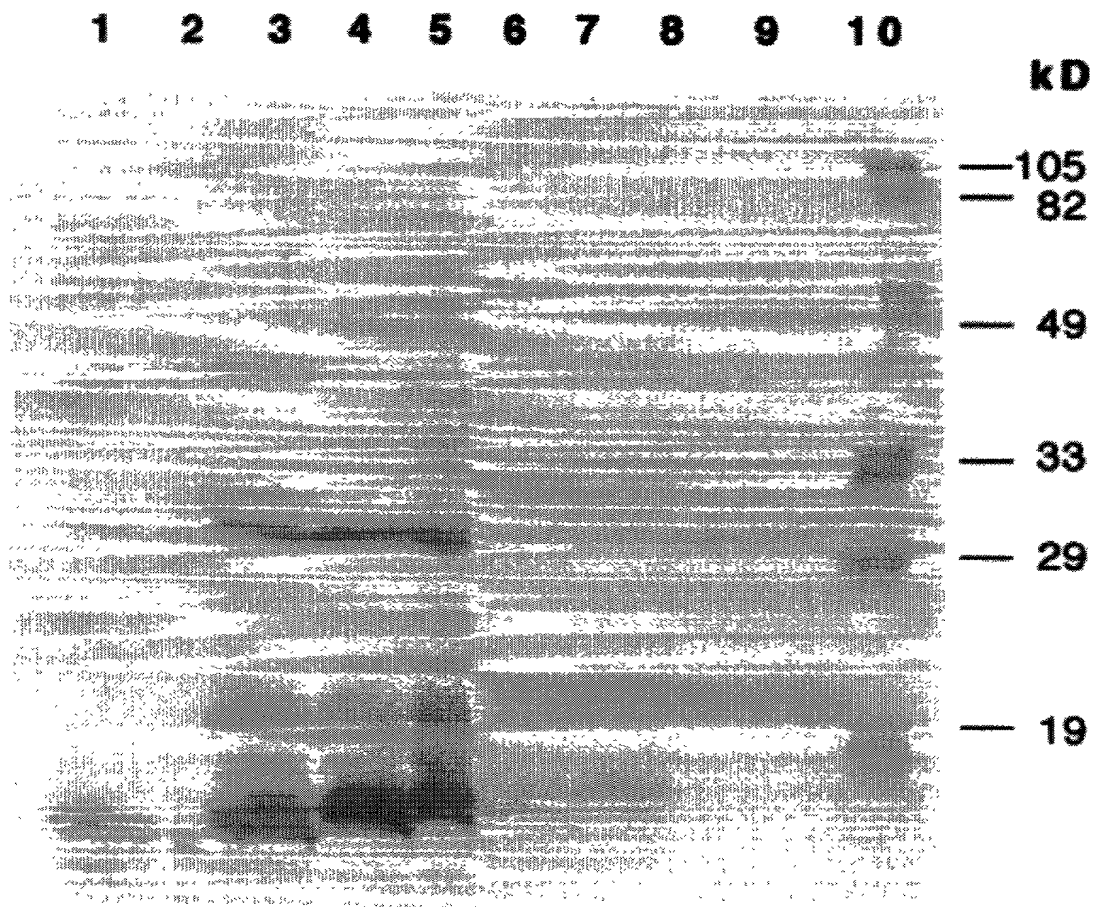


Fig 2.11

364960

Tm 12.86		L	T	D	E	Q	I	Q	K	R	N	K	I	S	K	E	?	Q	Q	V											
Tm 13.17	1	L	T	E	A	Q	I	E	K	L	N	K	I	S	K	K	C	Q	N	E	S	G	V	S	Q	E	I	I	T	K	A
B1	13	I	T	E	E	D	L	E	L	L	R	Q	T	S	A	E	C	K	T	E	S	G	V	S	E	D	V	I	K	R	A
AFP-3	1	E	T	P	R	E	K	L	K	Q	H	S	D	A	C	K	A	E	S	G	V	S	E	E	S	L	N	K	V		
Tm13.17	31	R	N	G	D	W	E	D	D	P	K	L	K	R	Q	V	F	C	V	A	R	N	A	G	L	A	T	E	S	G	E
B1	44	R	K	G	D	L	E	D	D	P	K	L	K	M	Q	L	L	C	I	F	K	A	L	E	I	V	A	E	S	G	E
AFP-3	29	R	N	R	E	E	V	D	D	P	K	L	K	E	H	A	F	C	I	L	K	R	A	G	F	I	D	A	S	G	E
Tm13.17	61	V	V	V	D	V	L	R	E	K	V	R	K	V	T	D	N	D	E	E	T	E	K	I	I	N	K	C	A	V	K
B1	75	I	E	A	D	T	F	K	E	K	L	T	R	V	T	N	D	D	E	E	S	E	K	I	V	E	K	C	T	V	T
AFP-3	59	F	Q	L	D	H	I	K	T	K	F	K	E	N	S	E	H	P	E	K	V	D	D	L	V	A	K	C	A	V	K
Tm13.17	91	R	D	T	V	E	E	T	V	F	N	T	F	K	C	V	M	K	N	K	P	K	F	S	P	V	D				
B1	106	E	D	T	P	E	D	T	A	F	E	V	T	K	C	V	L	K	D	K	P	N	F	F	G	D	L	F	V		
AFP-3	89	K	D	T	P	Q	H	S	S	A	D	F	F	K	C	V	H	D	N	R	S										

Fig. 2.12

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig. 3.0

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

Fig 3.1

Start



2-2	G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T G C	G
2-3	G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T G C	T
2-2	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G	
2-3	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G	
2-2	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A	
2-3	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A	
2-2	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C	
2-3	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C	
2-2	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A	T
2-3	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A	C
2-2	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C	
2-3	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C	
2-2	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G	
2-3	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G	
2-2	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G	
2-3	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G	
2-2	A A G A	G
2-3	A A G A	A
2-2	A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C	
2-3	A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C	
2-2	A A G T G T A T T T A C G A C A G	C
2-3	A A G T G T A T T T A C G A C A G	T
2-2	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A	
2-3	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A	
2-2	T A A A G G T A	A
2-3	T A A A G G T A	C

Fig 3.2

Predicted Amino Acid

Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 3.3

Lane	Protein	MW (kDa)
A	Protein A	17.8
B	Protein B	17.8
C	Protein C	17.8
D	Protein D	17.8
E	Protein E	17.8
F	Protein F	17.8

Fig. 3.4

20212019529660

Lane

1 2 3 4 5

a → ← a 577 bp
b → ← b 483 bp

Fig. 4.0

2007-2008 96292850

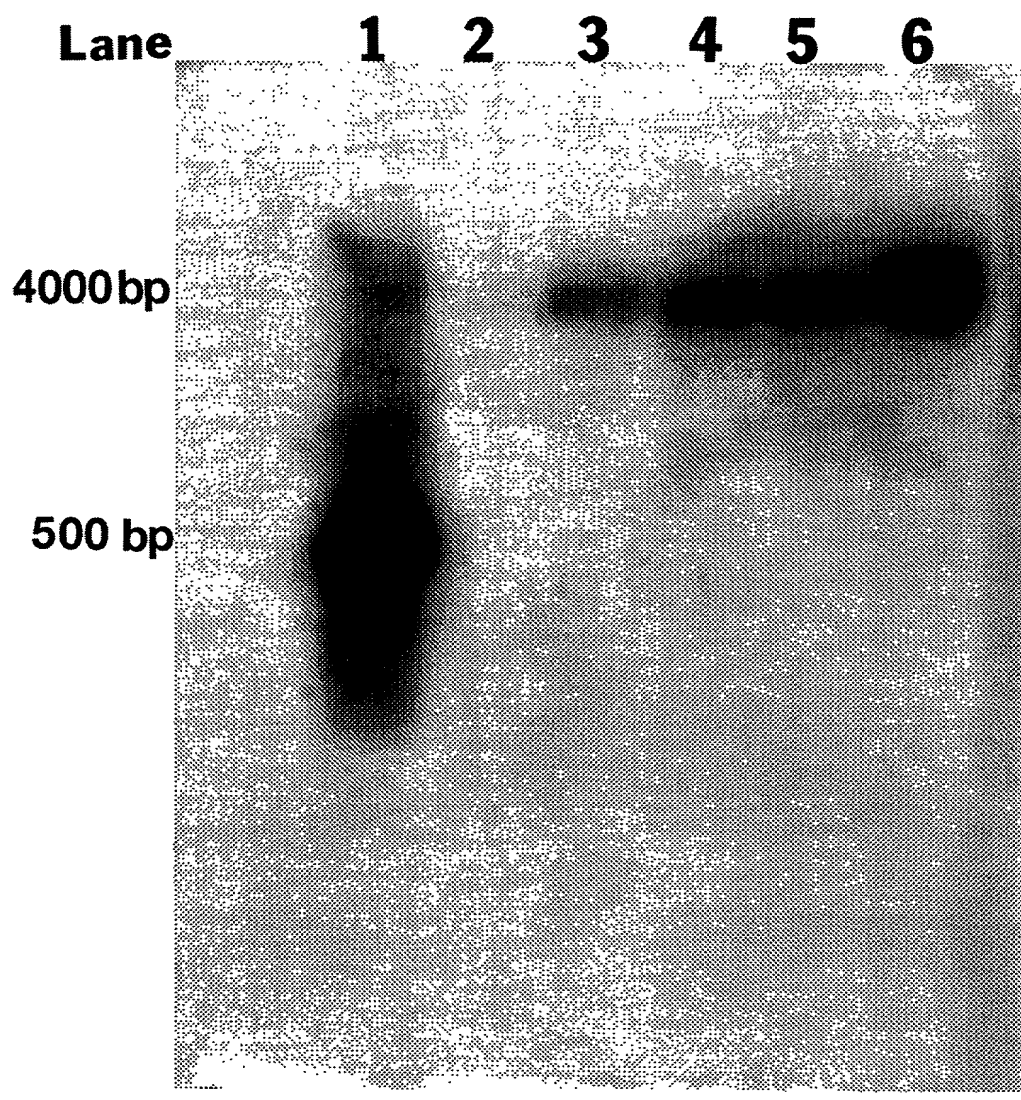


Fig. 4.1

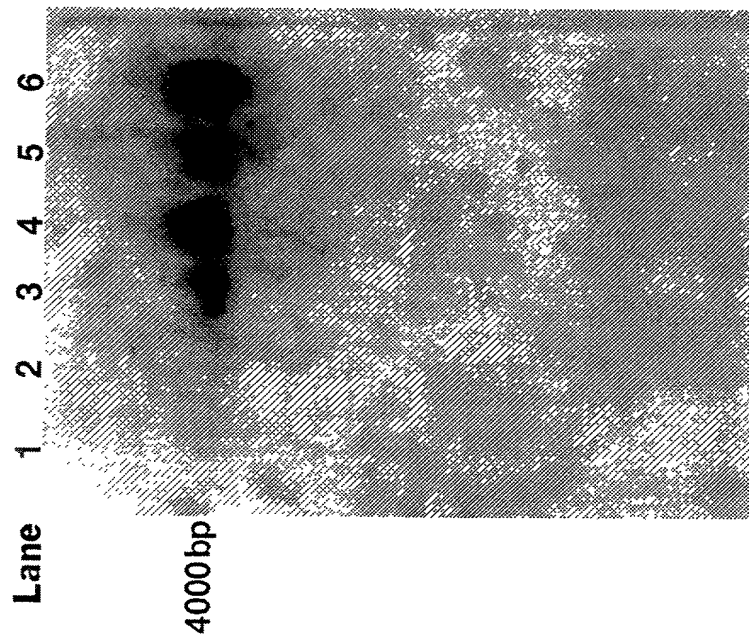
Lane 1 2 3 4 5 6

4000 bp

500 bp

Fig. 4.2

A.



B.

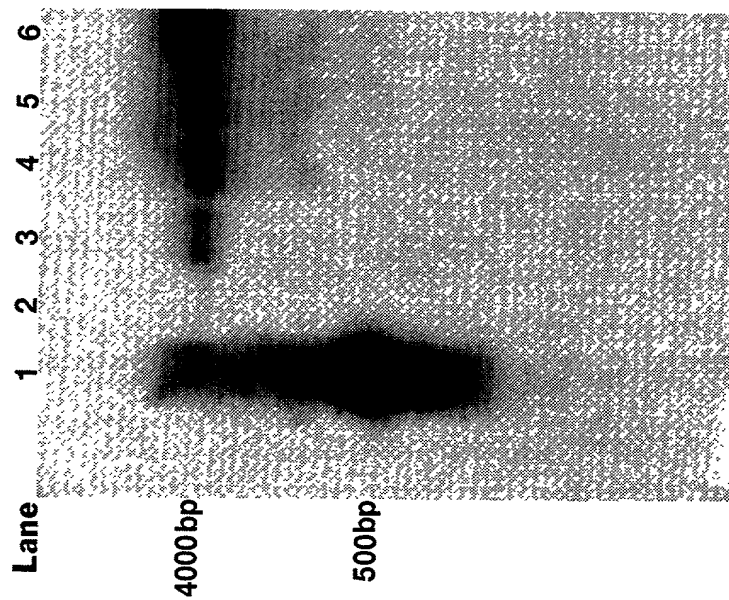


Fig. 4.3

Lane 1 2 3 4 5 6

4000 bp—

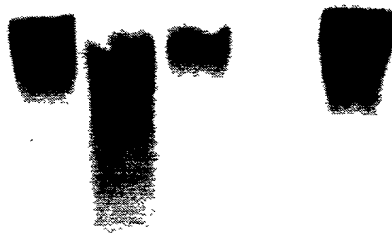


Fig. 4.4

2025-06-20 06:20:00

Lane

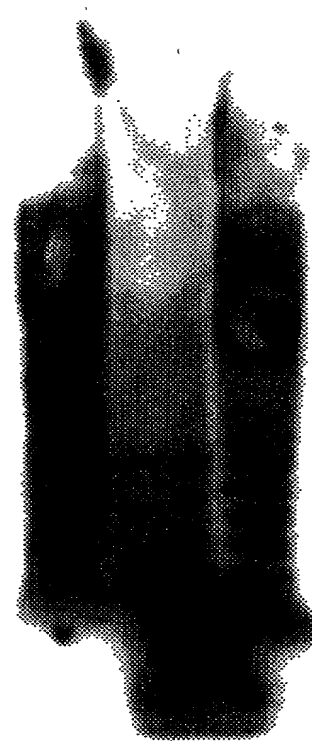
1

2

3

4

5



23130

9416

4361

2322

2027

564

Fig. 4.5

Tm 13.17 cDNA

1 AGTGGATCCAAAGAATTCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K
Forward Primer

121 AGATCAGCAAAAAATGTCAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTCGCTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R
Reverse Primer

361 GAGATACTGTTGAAGAGACGGTGTTCAATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAATATAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTCCACCC

Fig. 4.6a

Forward Primer

2-2 LTDEQIQKRNKISKECQQVS **GVSQET** IDKVRTGVLV
Tm 13.17 LTEAQIEKLNKISKKQNES **GVSQEI** ITKARNGDWE
B2 LTEEDLQLLRQTSAECKTES **GASEA** VIKKARKGDLE
AFP-3 ETPREKLKQHS DACKAES **GVSEE** SLNKVRNREEV

2-2 DDPKMKKHVLCFSKKTGVATEAGDTNVEVLKAKLKH
Tm 13.17 DDPKLKRQVFCVARNAGLATESGEVVVDVLREKVRK
B2 DDPKLKMQLLCIFKALEIVAESGEIEADTFKEKLTR
AFP-3 DDPKLKEHAFCLKRAGFIDASGEFQLDHIKTKFKE

Reverse Primer

2-2 VAS DEEVDKIVQKCVVKK **ATPEET** AYDTFKCIYDS
Tm 13.17 VTDNDEETEKIINKCAVKR **DTVEET** VFNTFKCVMKN
B2 VTNDDEESEKIVEKCTVTE **DTPEDT** AFEVTKCVLKD
AFP-3 NSEHPEKVDDLVAKCAVKK **DTPQHS** SADFFKCVHDN

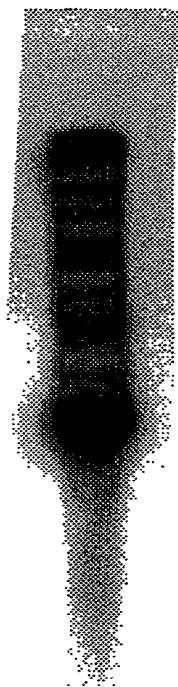
2-2 KPDFSPI D
Tm 13.17 KPKFSPVD
B2 KPNFFGDLFV
AFP-3 RS

Fig. 4.6b

Primer	percent % composition				Melting Temperature(°C)
	A	C	G	T	
Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

Fig. 4.6c

09876543210



3600 bp

Fig. 4.7

0906796.02200

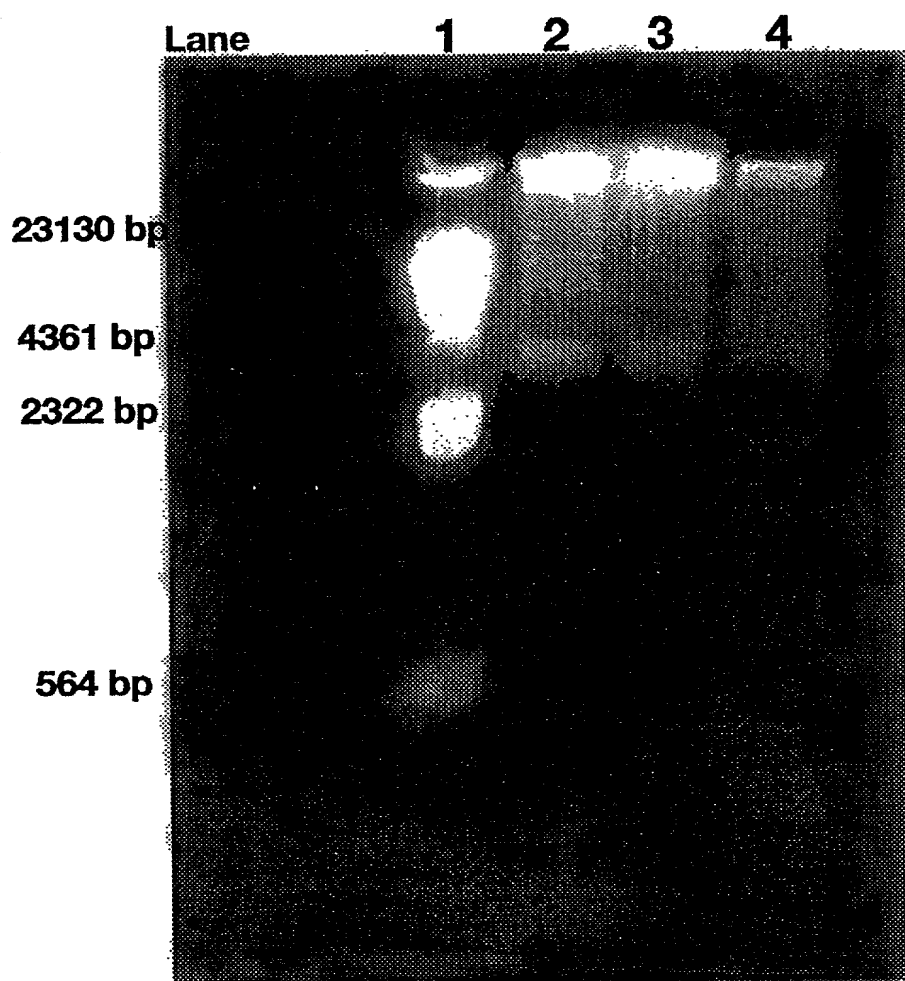


Fig. 4.8

09876543210

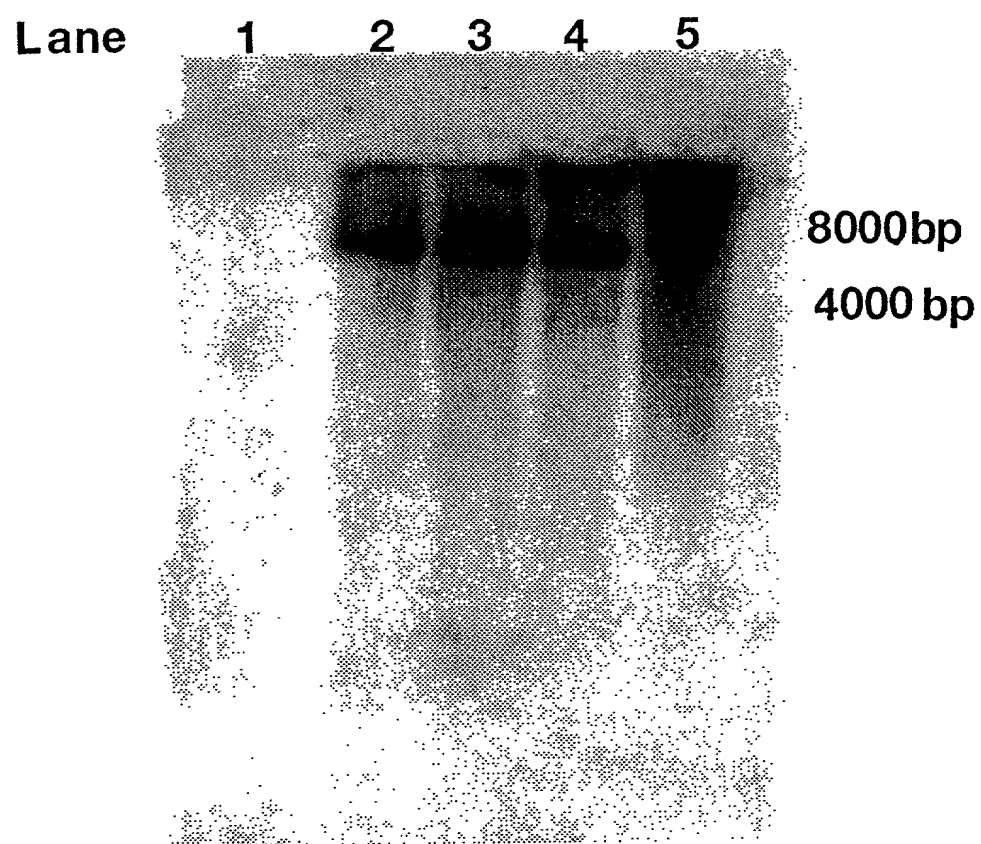


Fig. 4.9

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCTTTGCGCCGCC
 M K L L L C F A F A A
 47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
 I V I G A Q A L T D E Q I Q K
 92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
 R N K I S K E C Q Q V S G V S
 137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
 Q E T I D K V R T G V L V D D
 182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
 P K M K K H V L C F S K K T G
 226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
 V A T E A G D T N V E V L K A
 271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
 K L K H V A S D E E V D K I V
 316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
 Q K C V V K K A T P E E T A Y
 361 GACACCTTCAAGGTTATTTACGACAGTAAACCTGATTTCTCTCCT
 D T F K V I Y D S K P D F S P
 406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
 I D *
 451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA polyadenylation signal

poly (A) tail

Fig. 4.10a

Predicted Amino Acid

Composition of 3-4

Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AILFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.10b

polyadenylation signal

Fig. 4.11a

Fig. 4.11a

Predicted Amino Acid

Composition of 3-9

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.11b

polyadenylation signal

Fig. 4.12a

Fig. 4.12a

Predicted Amino Acid

Composition of 7-5

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

Fig. 4.12b



2-2
2-3
3-4
3-9
7-5

MKLLLCFAFAAIVIGAAQALTDEQIQKRNKISKKECCQQVSGVSSQETIDKVRTTGGVLLV
MKLLLCFAFAAIVIGAAQALTDEQIQKRNKISKKECCQQVSGVSSQETIDKVRTTGGVLLV
MKLLLCFAFAAIVIGAAQALTDEQIQKRNKISKKECCQQVSGVSSQETIDKVRTTGGVLLV
MKLLLCFAFAAIVIGAAQALTDEQIQKRNKISKKECCQQVSGVSSQETIDKVRTTGGVLLV

2-2
2-3
3-4
3-9
7-5

DDPKMKKHHVLCFSSKKKTGGVATEAGDTNVEVLLKAKLLKHHVASDEEEVDDKIVQQKCCVVKK
DDPKMKKHHVLCFSSKKKTGGVATEAGDTNVEVLLKAKLLKHHVASDEEEVDDKIVQQKCCVVKK
DDPKMKKHHVLCFSSKKKTGGVATEAGDTNVEVLLKAKLLKHHVASDEEEVDDKIVQQKCCVVKK
DDPKMKKHHVLCFSSKKKTGGVATEAGDTNVEVLLKAKLLKHHVASDEEEVDDKIVQQKCCVVKK

2-2
2-3
3-4
3-9
7-5

ATPEETAYDTEFFKCIYDSKPPDFSPID*
ATPEETAYDTEFFKCIYDSKPPDFSPID*
ATPEETAYDTEFFKCIYDSKPPDFSPID*
ATPEETAYDTEFFKCIYDSKPPDFSPID*

Fig. 4.14

	MW (kDa)	AA (#)	(% mole)										% most hydrophobic	(% mole)										% most hydrophilic
			Cys	Pro	Phe	Ile	Val	Met	Leu	Gly	Ala	Tyr		His	Trp	Asx	Glx	Arg	Lys	Ser	Thr			
Tm 12.86	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3	57.3		
Tm 13.17	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.41	0	0	7.12	15.6	3.31	6.14	32.14		
2-2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23		
2-3	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23		
3-4	12.84	115	2.41	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.09	32.24		
3-9	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07	32.38		
7-5	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23		

Fig. 4.15

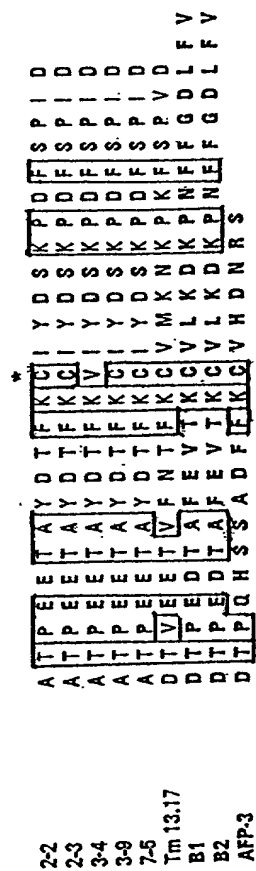
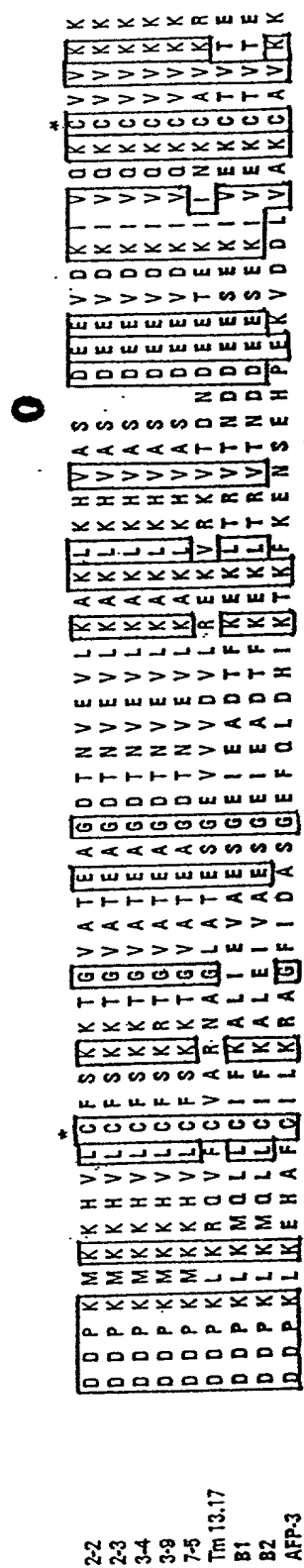
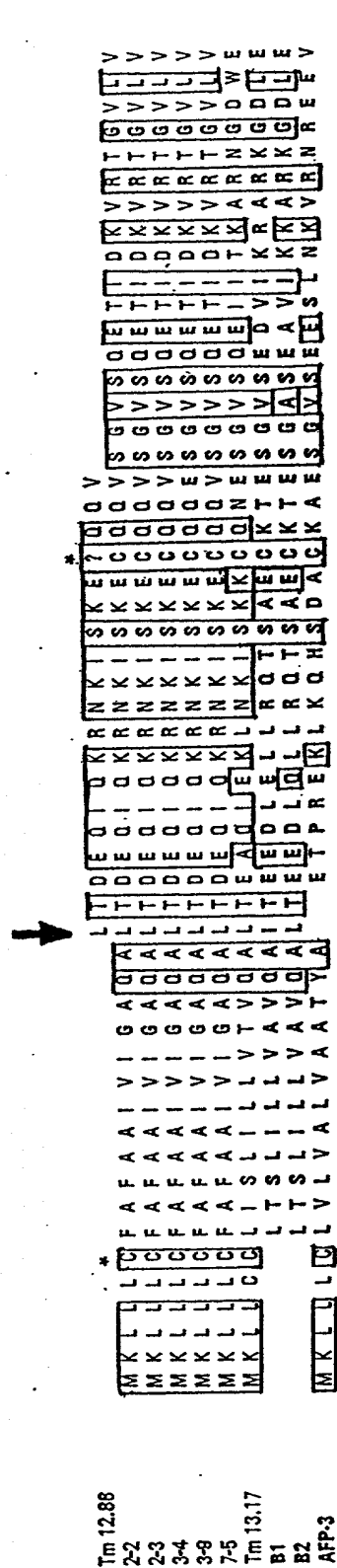
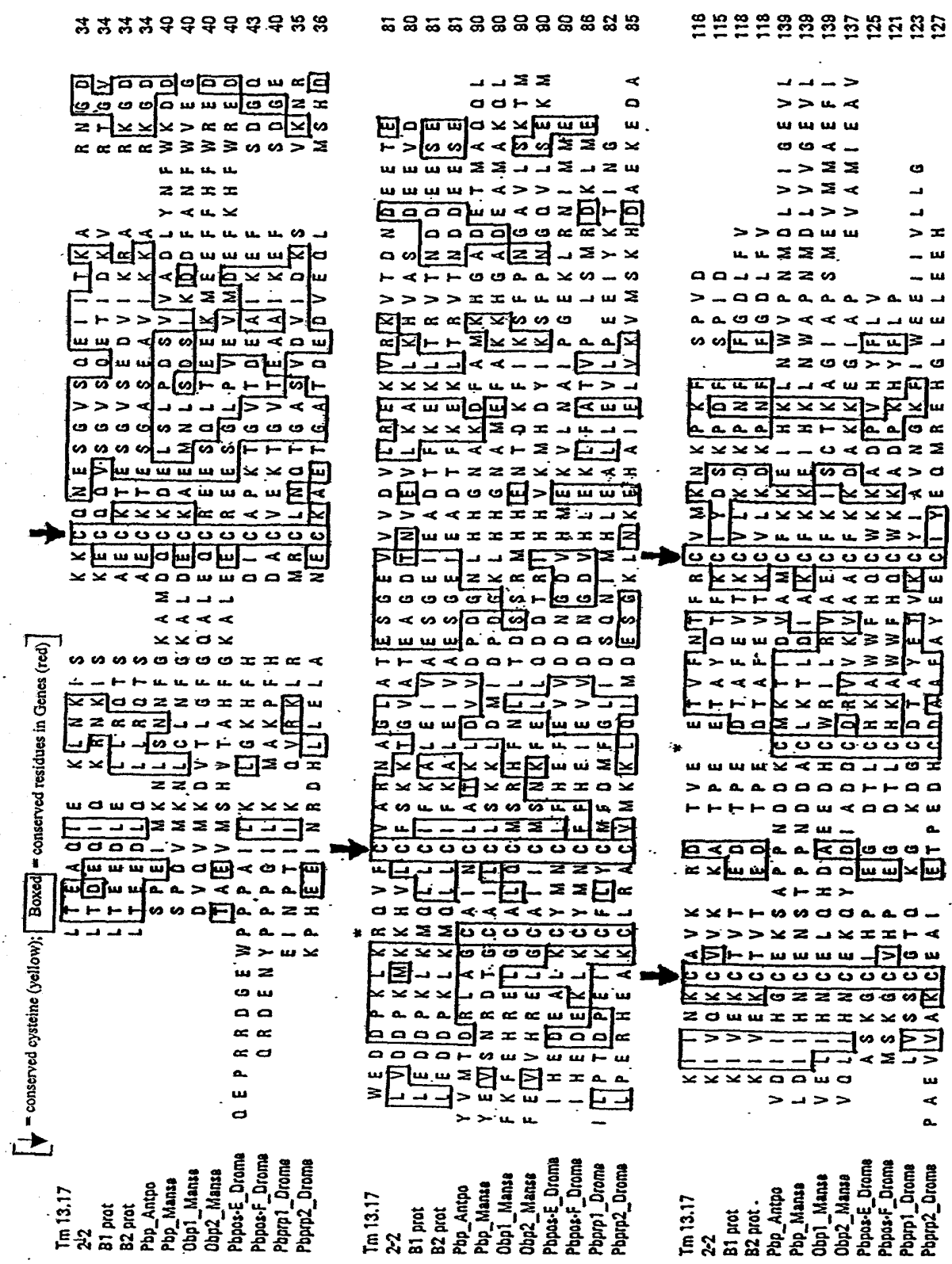


FIG 4.16
* = conserved cysteine (yellow)

Boxed = conserved residues in ≥ 7 Genes (blue or orange)

Fig. 4.16



NUCLEOTIDE SEQUENCES

PERCENT SIMILARITY

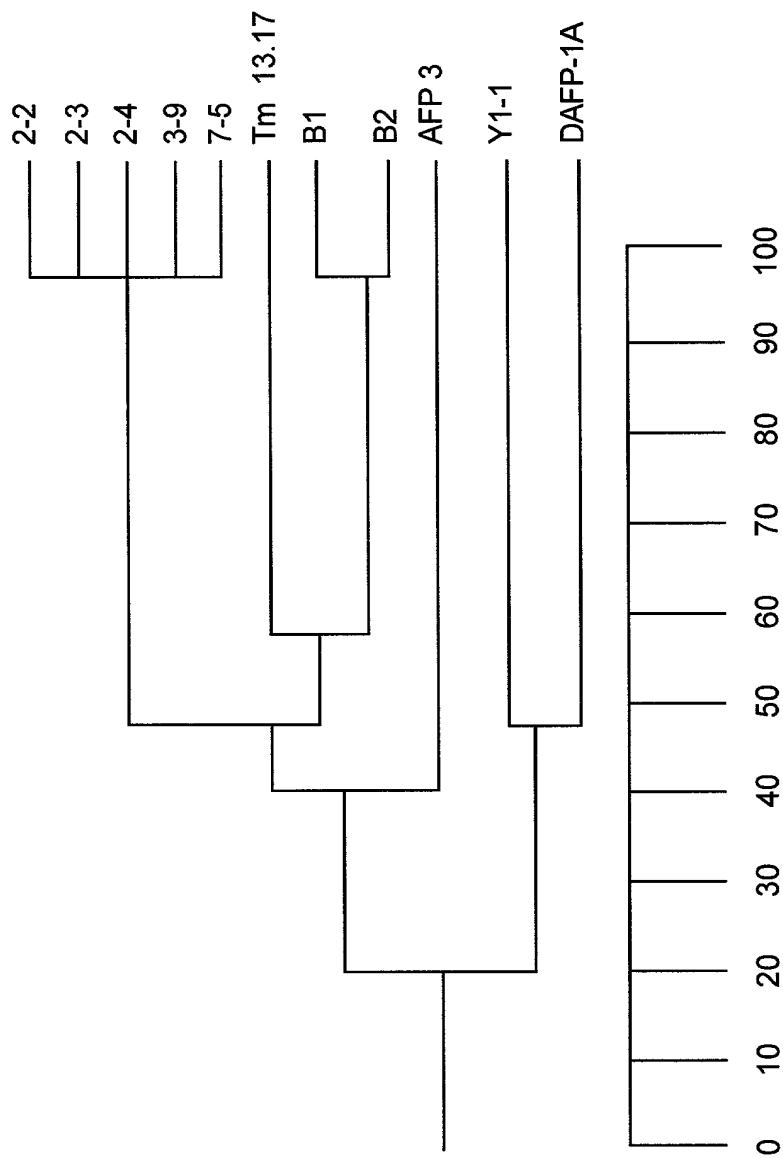
	1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}		
PERCENT DIVERGENCE	1	2	3	4	5	6	7	8	9	10	1	2-2
1		99.1	97.3	98.4	98.2	50.4	42	42.4	20.7	20.9	1	2-2
2	0.9		99	99	99	51.5	43.2	42.7	20.2	21.3	2	2-3
3	1.6	60		98	98	50.3	42	42.1	20	20	3	3-4
4	1.6	20	80		98.4	51.3	43.7	43.6	20.4	22	4	3-9
5	1.8	25	75	45		50.4	42.5	42.9	22.2	23.1	5	7-5
6	36.9	36.4	37.2	36.4	37.1		57.2	37.4	23.3	21	6	Tm 13.17
7	39.9	41.2	41.7	40.7	41.2	30.2		39.3	21.9	22.1	7	B1
8	41.8	42.4	43.1	42.3	42.3	45.3	49.4		21.8	23.1	8	AFP-3
9	48.7	58.6	52	51.2	51.9	61.7	62.2	58.2		45.6	9	YL-1
10	51.4	62.7	46.4	46.5	46.5	60	58.1	61.8	35.5		10	DAFP-1A
	1	2	3	4	5	6	7	8	9	10		

AMINO ACID SEQUENCES

PERCENT SIMILARITY

	1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}		
PERCENT DIVERGENCE	1	2	3	4	5	6	7	8	9	10	1	2-2
1		100	99.1	99.1	100	51.3	37.4	35.2	11.6	12	1	2-2
2	0		99.1	99.1	100	51.3	37.4	35.2	11.6	12	2	2-3
3	0.9	0.9		98.3	99.1	50.4	36.5	34.3	11.6	12	3	3-4
4	0.9	0.9	1.7		99.1	51.3	37.4	36.1	10.7	12	4	3-9
5	0	0	0.9	0.09		51.3	37.4	35.2	11.6	12	5	7-5
6	46.1	46.1	47	46.1	46.1		47.4	39.8	13.4	13.9	6	Tm 13.17
7	59.1	59.1	60	59.1	59.1	51.7		37	11.6	11.1	7	B1
8	61.7	61.7	62.6	60.7	61.7	60.2	63		10.2	8.3	8	AFP-3
9	86.7	86.7	85.7	85.7	85.7	86.8	84.2	87.5		55.6	9	YL-1
10	88.3	88.3	86.4	84.5	85.4	89.1	82.7	90.5	40.2		10	DAFP-1A
	1	2	3	4	5	6	7	8	9	10		

Fig. 4.19



% Nucleic Acid Identity

Fig. 4.20

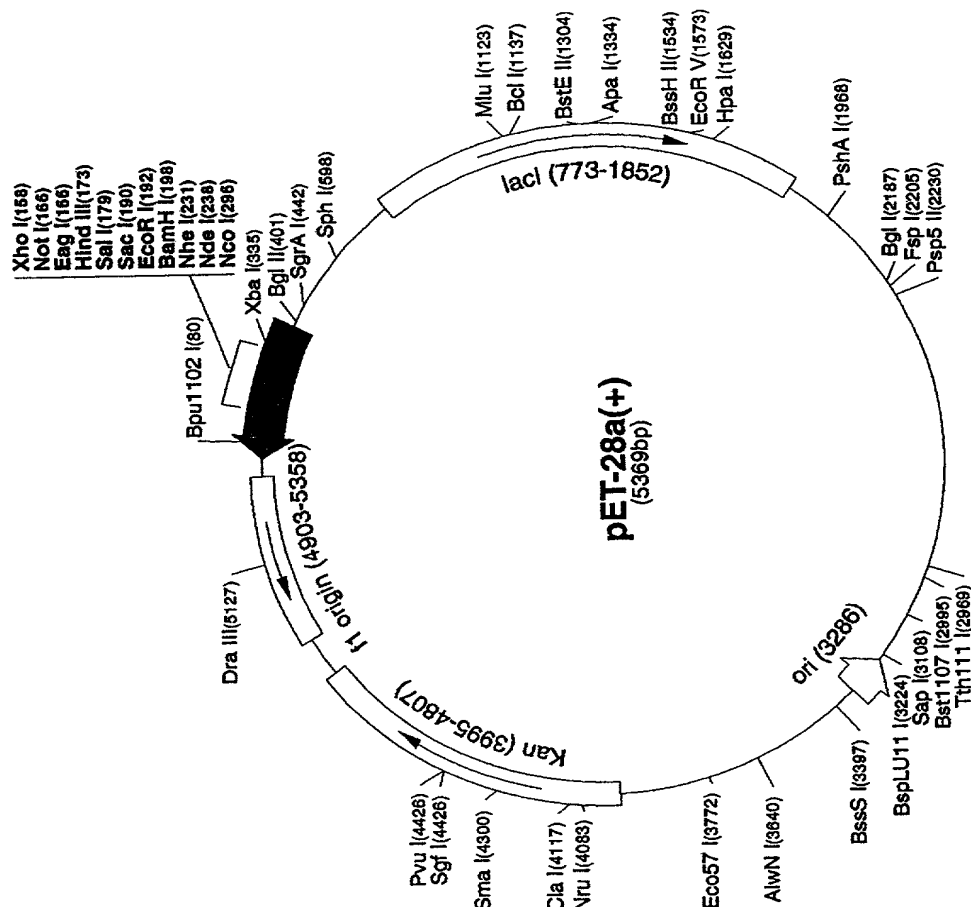


Fig. 5.0

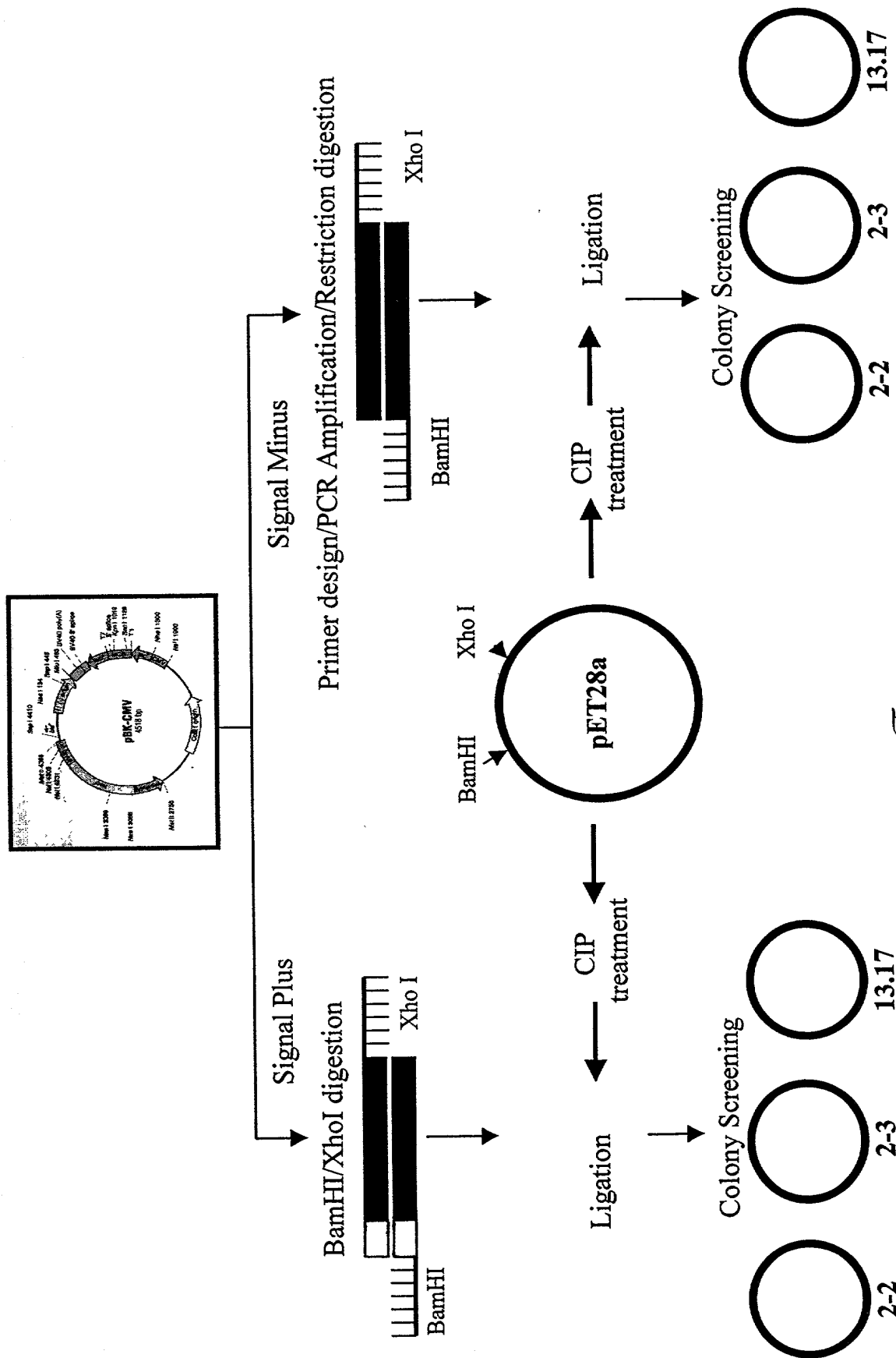


Fig. 5.1

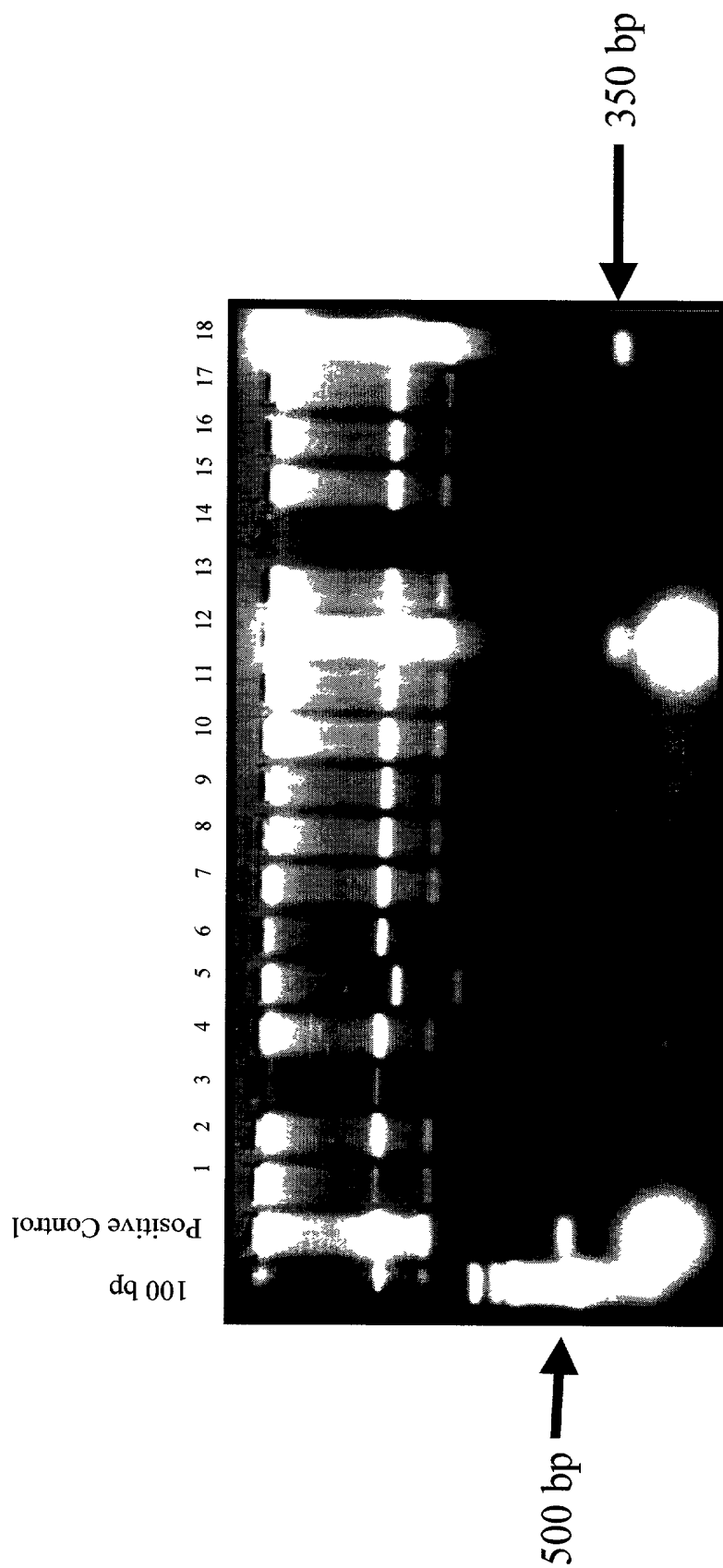


Fig. 5.2

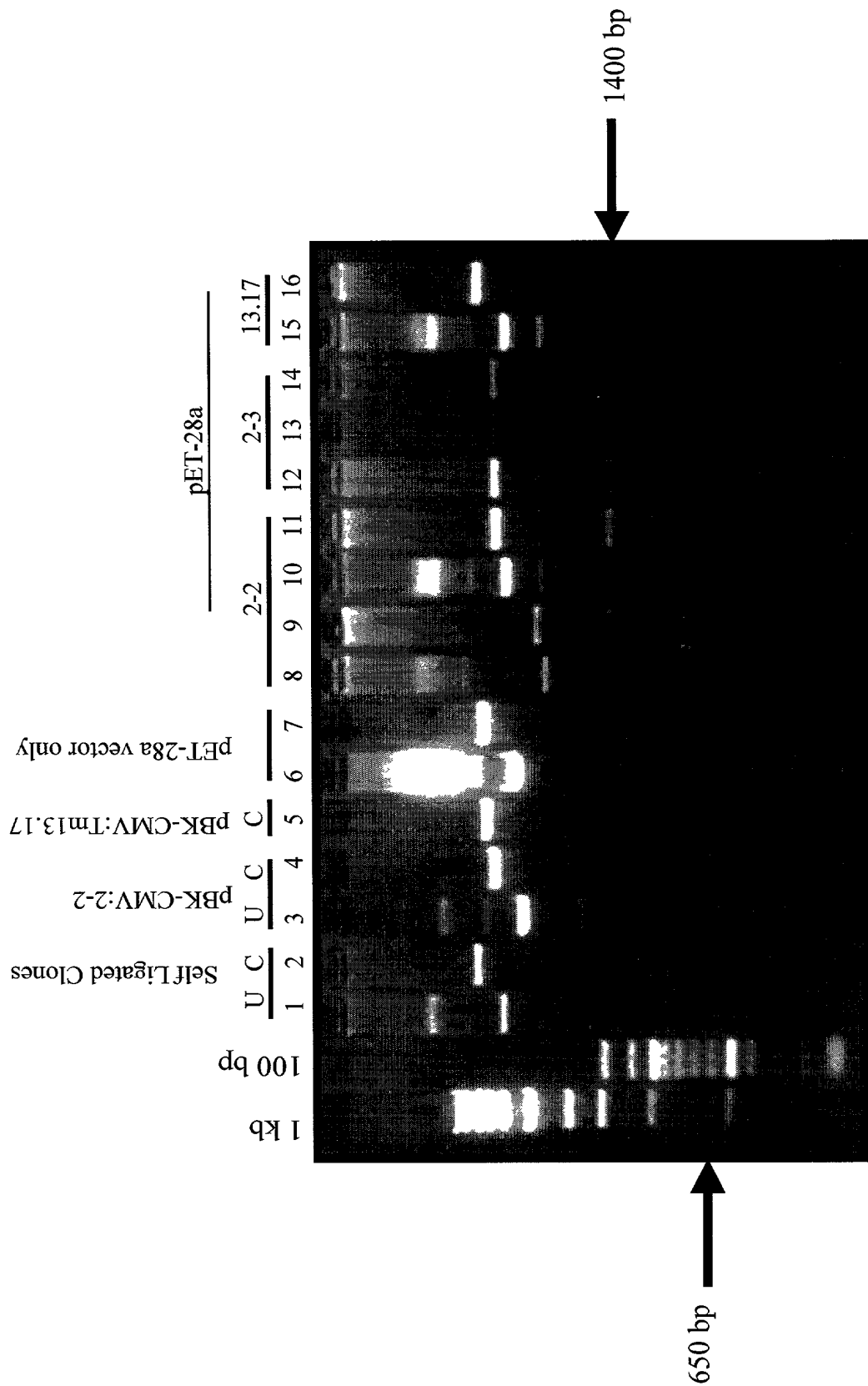


Fig. 5.3

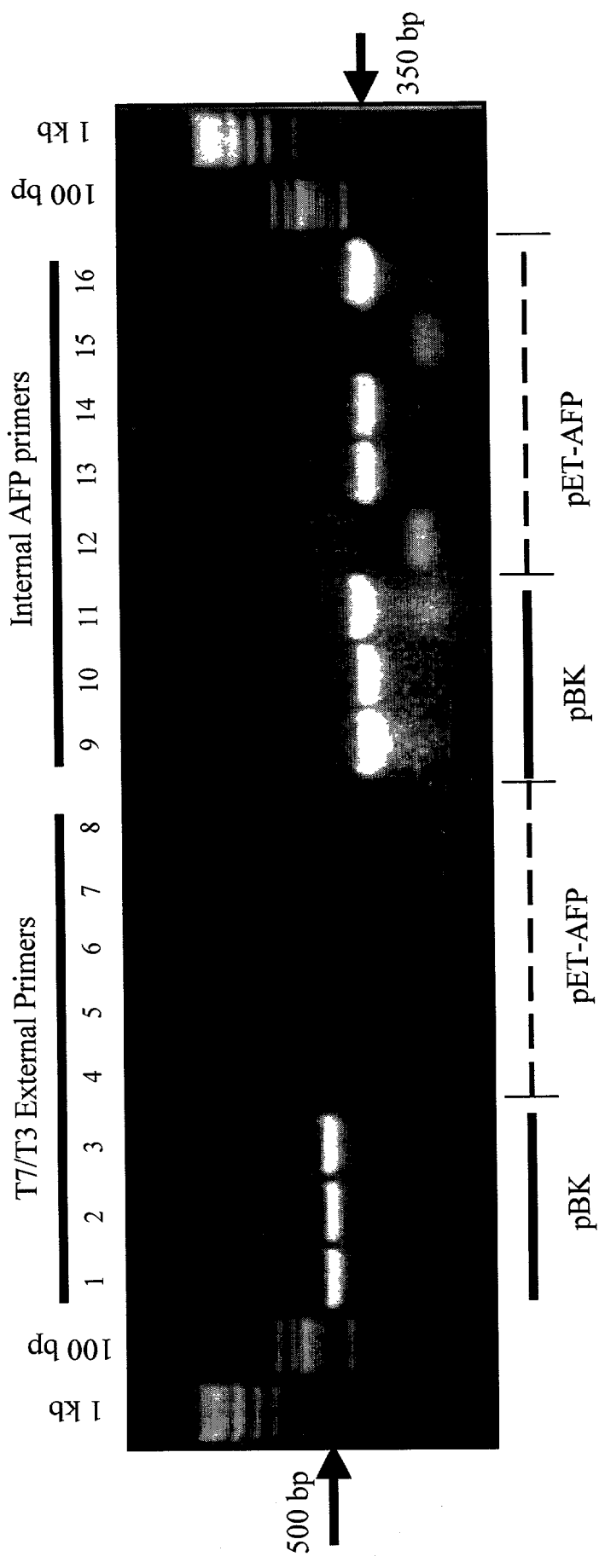


Fig. 5.4

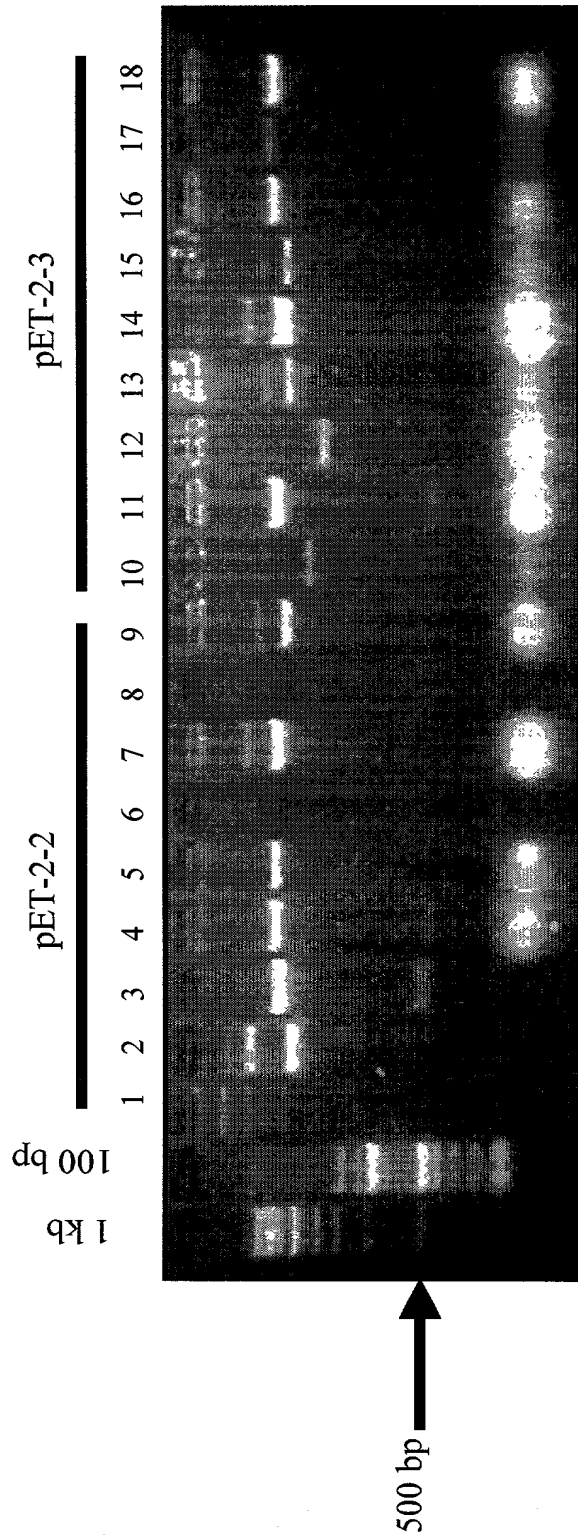


Fig. 5.5

20090926

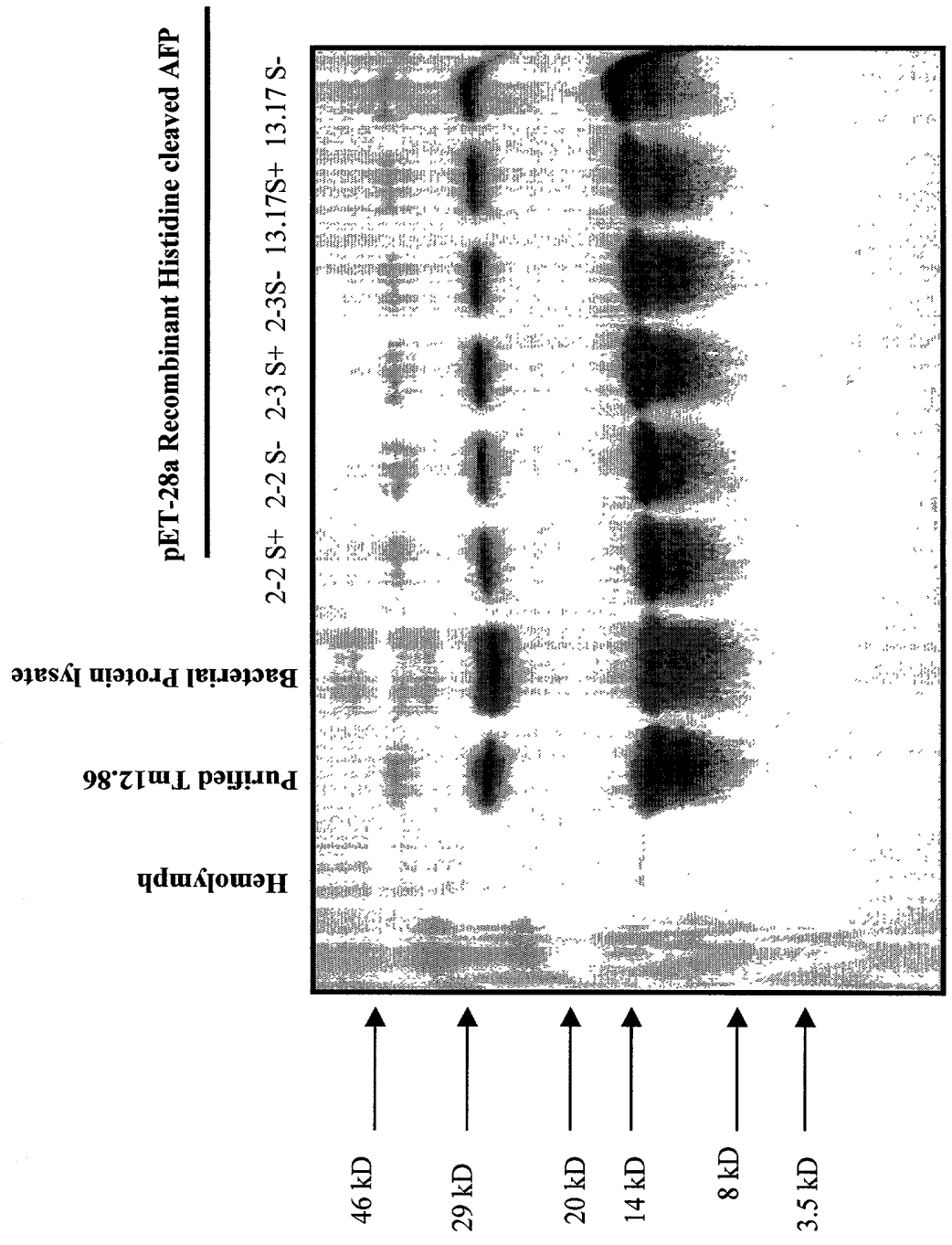


Fig 5.6

His-tagged Clone 2 2 with signal sequence

TTGTTAGCGG ATGGAATTC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AFP Start Codon	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
N-terminal of mature AFP	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
Stop Codon	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
Polyadenylation signal Poly-A tail	
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAATCG AGCACCACCA CCACCACCAC TGAGAT	681

Fig. 5.7

His-tagged clone 2.2 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
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Fig. 5.8

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Fig. 5.9

His-tagged Clone 2.3 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCAC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

Fig. 5.10

His-tagged Tm 13 17 with signal sequence		
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	CTTAAAG	50
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC		96
Met Gly Ser Ser His His His His His Ser		
-65	-60	-55
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT		141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-50	-45	-40
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT		186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile		
-35	-30	-25
AFP Start Codon		
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC		231
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser		
-20	-15	-10
N-terminal of mature AFP		
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT		276
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile		
-5	1	5
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA		321
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly		
10	15	20
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG		366
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu		
25	30	35
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC		411
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn		
40	45	50
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG		456
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu		
55	60	65
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG		501
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu		
70	75	80
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG		546
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu		
85	90	95
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG		595
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys		
100	105	110
Stop Codon		
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG		643
Phe Ser Pro Val Asp *		
115		
Polyadenylation signal Poly-A tail		
TGTGCTTTAC ATATAAAAT AAAGTGTTC TGATGTAAAA AAAAAAAAAA		693
AAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT		743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT		777

Fig. 5.11

His-tagged Tm 13.17 without signal sequence			
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG			50
His-tag Start Codon			
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC			96
Met Gly Ser Ser His His His His His His Ser			
-30		-25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT			141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly			
-20		-15	-10
N-terminal of mature AFP			
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA			186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys			
-5	1	5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG			231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser			
10	15	20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT			276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp			
25	30	35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT			321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly			
40	45	50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG			366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu			
55	60	65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC			411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile			
70	75	80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG			456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val			
85	90	95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA			501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser			
100	105	110	
Stop Codon			
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT			543
Pro Val Asp *			
115			

Fig. 5.12

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MW(KD)

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94.0

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14.4

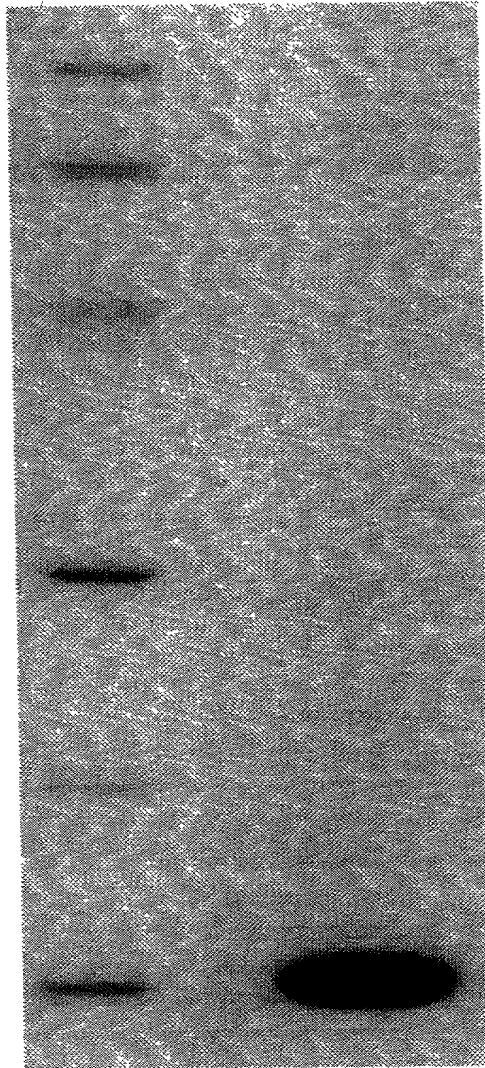


Fig. 6.0

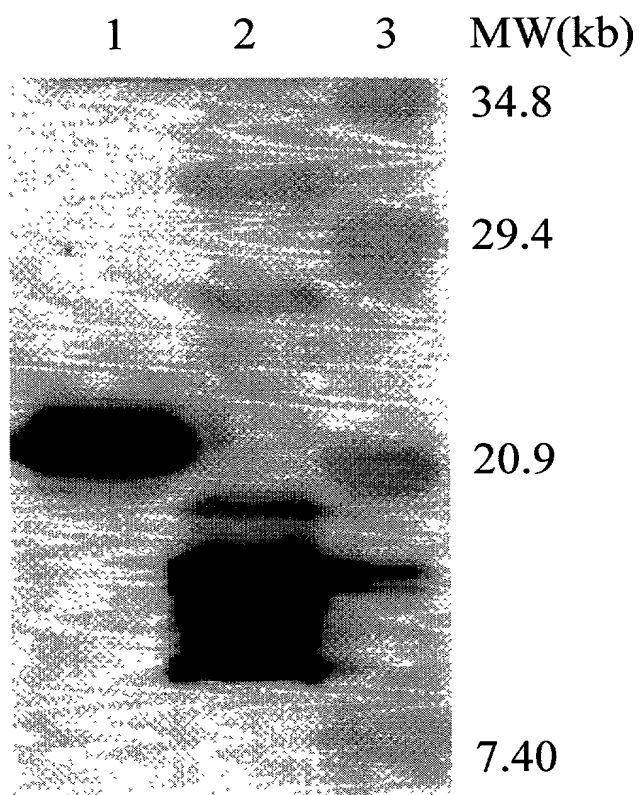


Fig. 6.1

Figure 1 consists of four black and white micrographs labeled A, B, C, and D, arranged in a 2x2 grid. Micrographs A and B show cross-sections of plant tissue with large, polygonal cells and prominent, dark-stained nuclei. Micrograph C shows a similar tissue structure but with cells containing dark, granular cytoplasm. Micrograph D shows cells with large, clear, vacuolated cytoplasm, indicating a different physiological state or treatment effect.

Fig. 6.2

Tm 13.17 S-graph data

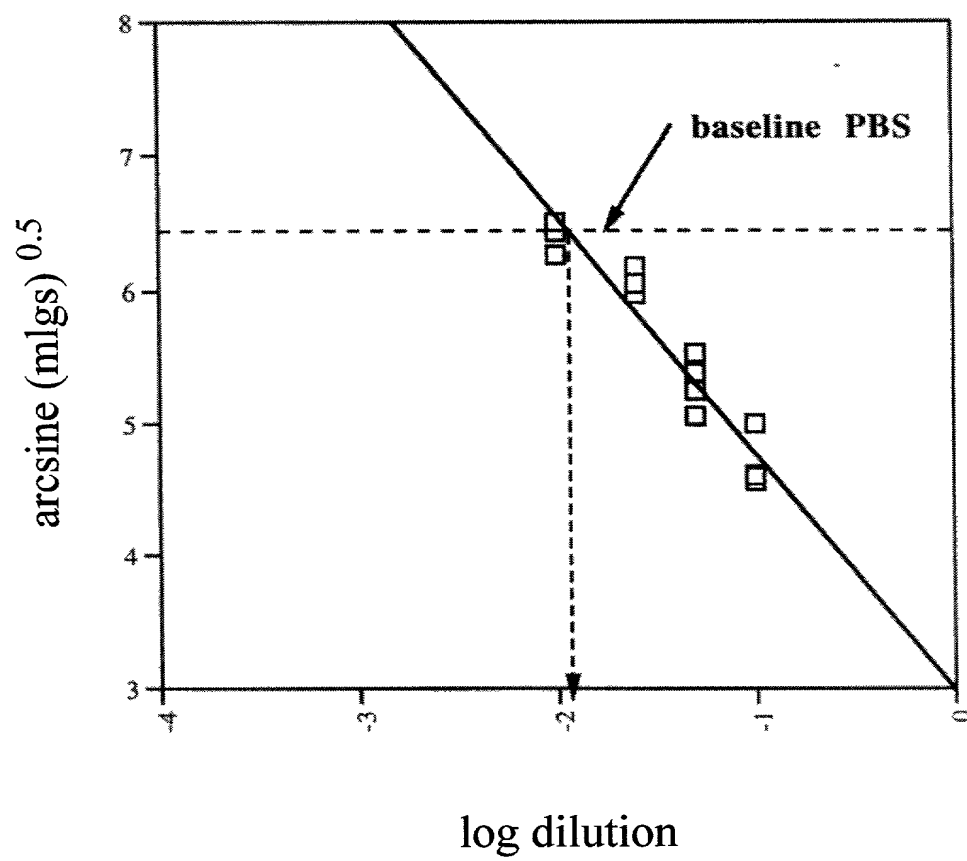


Fig. 6.3

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulfhydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulfhydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

Fig. 7.1

Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Consensus of Tm12 84	Tm13 17	Consensus with Tm 13 17	B1	Consensus with B1	AFP-3	Consensus with AFP-3
1	A	A	A	A	A	A	A	A		A	C	C
2	C	G	G	G	G	C	G	N		N	A	N
3	G	A	A	A	A	G	A	R		R	G	R
4	A	G	G	G	G	C	C	N		N	A	N
5	G	C	C	C	C	G	T	N		N	T	N
6	C	A	A	A	A	C	A	N		N	C	N
7	A	A	A	A	A	A	C	N		N	C	N
8	A	A	A	A	A	A	T	N		N	G	N
9	A	A	A	A	A	A	A	A		A	A	A
10	A	A	A	A	A	A	A	R		A	G	A
11	A	A	A	A	A	A	G	R		A	G	A
12	A	A	A	A	A	A	A	R		A	G	A
13	A	A	A	A	A	A	A	R	A?	A	A	A
14	T	G	A	A	G	T	G	A	T?	T	A	T
15	G	A	A	A	A	G	A	A	G	A	G	A
16	A	A	A	A	A	A	A	A	A	A	A	A
17	A	A	A	A	A	A	A	A	A	A	A	A
18	A	A	A	A	A	A	A	A	A	A	A	A
19	C	A	A	A	A	A	G	R		R	G	R
20	T	C	C	C	C	C	T	Y		Y	C	C
21	C	C	C	C	C	C	T	C	C/G	C/G	C	C/G
22	C	C	C	C	C	C	T	C	C	C	O	O
23	T	T	T	T	T	T	T	N		N	T	T
24	T	T	T	T	T	T	T	N		N	C	C
25	T	T	T	T	T	T	T	N		N	T	T
26	T	T	T	T	T	T	T	N		N	T	T
27	T	T	T	T	T	T	T	N		N	T	T
28	T	T	T	T	T	T	T	N		N	T	T
29	T	T	T	T	T	T	T	N		N	T	T
30	T	T	T	T	T	T	T	N		N	T	T
31	T	T	T	T	T	T	T	N		N	T	T
32	T	T	T	T	T	T	T	N		N	T	T
33	T	T	T	T	T	T	T	N		N	T	T
34	T	T	T	T	T	T	T	N		N	T	T
35	T	T	T	T	T	T	T	N		N	T	T
36	T	T	T	T	T	T	T	N		N	T	T
37	T	T	T	T	T	T	T	N		N	T	T
38	T	T	T	T	T	T	T	N		N	T	T
39	T	T	T	T	T	T	T	N		N	T	T
40	T	T	T	T	T	T	T	N		N	T	T
41	T	T	T	T	T	T	T	N		N	T	T
42	T	T	T	T	T	T	T	N		N	T	T
43	T	T	T	T	T	T	T	N		N	T	T
44	T	T	T	T	T	T	T	N		N	T	T
45	T	T	T	T	T	T	T	N		N	T	T
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49	T	T	T	T	T	T	T	N		N	T	T
50	T	T	T	T	T	T	T	N		N	T	T
51	T	T	T	T	T	T	T	N		N	T	T
52	T	T	T	T	T	T	T	N		N	T	T
53	T	T	T	T	T	T	T	N		N	T	T
54	T	T	T	T	T	T	T	N		N	T	T
55	T	T	T	T	T	T	T	N		N	T	T
56	T	T	T	T	T	T	T	N		N	T	T
57												

Fig. 7.2

20250323 14:26:59

Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Concensus of	Tm13 17	Concensus with	B1	Concensus with	AFF-3	Concensus with
118	C	C	C	C	C	C	A	N	A	N	G	N
119	A	A	A	A	A	A	A	N	C	N	G	N
120	G	G	G	G	G	G	T	N	T	N	G	N
121	G	G	G	G	G	G	G	G	A	G	A	A
122	T	T	T	T	T	T	A	T/A	R	T/A	R	T/A
123	T	T	T	T	T	T	G	C/G	C/G	C/G	C	C/G
124	C	C	C	C	C	C	G	G	G	G	G	G
125	C	C	C	C	C	C	A	T	A	A	A	A
126	G	G	G	G	G	G	G	G	G	G	G	G
127	A	A	A	A	A	A	A	T	T	T	T	T
128	G	G	G	G	G	G	G	G	G	G	G	G
129	A	A	A	A	A	A	A	G	A	A	A	A
130	G	G	G	G	G	G	G	T	G	G	G	G
131	T	T	T	T	T	T	T	T	T	T	T	T
132	T	T	T	T	T	T	C	C/G	C/G	C/G	C	C
133	C	C	C	C	C	C	C	C	C	C	C	C
134	C	C	C	C	C	C	A	A	A	A	A	A
135	C	C	C	C	C	C	A	A	A	A	A	A
136	C	C	C	C	C	C	A	A	A	A	A	A
137	A	A	A	A	A	A	A	A	A	A	A	A
138	A	A	A	A	A	A	A	A	A	A	A	A
139	G	G	G	G	G	G	A	A	A	A	A	A
140	A	A	A	A	A	A	A	A	A	A	A	A
141	G	G	G	G	G	G	A	A	A	A	A	A
142	A	A	A	A	A	A	A	A	A	A	A	A
143	C	C	C	C	C	C	A	A	A	A	A	A
144	G	G	G	G	G	G	A	A	A	A	A	A
145	A	A	A	A	A	A	A	A	A	A	A	A
146	T	T	T	T	T	T	A	A	A	A	A	A
147	C	C	C	C	C	C	A	A	A	A	A	A
148	G	G	G	G	G	G	A	A	A	A	A	A
149	A	A	A	A	A	A	A	A	A	A	A	A
150	C	C	C	C	C	C	A	A	A	A	A	A
151	A	A	A	A	A	A	A	A	A	A	A	A
152	A	A	A	A	A	A	A	A	A	A	A	A
153	A	A	A	A	A	A	A	A	A	A	A	A
154	G	G	G	G	G	G	T	T	T	T	T	T
155	T	T	T	T	T	T	C	C	C	C	C	C
156	C	C	C	C	C	C	C	C	C	C	C	C
157	G	G	G	G	G	G	C	C	C	C	C	C
158	C	C	C	C	C	C	C	C	C	C	C	C
159	C	C	C	C	C	C	A	A	A	A	A	A
160	A	A	A	A	A	A	A	A	A	A	A	A
161	C	C	C	C	C	C	A	A	A	A	A	A
162	A	A	A	A	A	A	C	C	C	C	C	C
163	G	G	G	G	G	G	G	G	G	G	G	G
164	G	G	G	G	G	G	T	T	T	T	T	T
165	T	T	T	T	T	T	G	G	G	G	G	G
166	T	T	T	T	T	T	A	A	A	A	A	A
167	T	T	T	T	T	T	C	C	C	C	C	C
168	T	T	T	T	T	T	G	G	G	G	G	G
169	T	T	T	T	T	T	G	G	G	G	G	G
170	T	T	T	T	T	T	G	G	G	G	G	G
171	G	G	G	G	G	G	G	G	G	G	G	G
172	T	T	T	T	T	T	C	C	C	C	C	C
173	T	T	T	T	T	T	G	G	G	G	G	G
174	C	C	C	C	C	C	A	A	A	A	A	A
175	G	G	G	G	G	G	A	A	A	A	A	A
176	A	A	A	A	A	A	A	A	A	A	A	A
177	T	T	T	T	T	T	A	A	A	A	A	A
178	G	G	G	G	G	G	A	A	A	A	A	A
179	A	A	A	A	A	A	A	A	A	A	A	A
180	T	T	T	T	T	T	C	C	C	C	C	C
181	C	C	C	C	C	C	C	C	C	C	C	C
182	C	C	C	C	C	C	A	A	A	A	A	A
183	C	C	C	C	C	C	A	A	A	A	A	A
184	A	A	A	A	A	A	A	A	A	A	A	A
185	A	A	A	A	A	A	A	A	A	A	A	A
186	A	A	A	A	A	A	A	A	A	A	A	A
187	A	A	A	A	A	A	A	A	A	A	A	A
188	T	T	T	T	T	T	G	G	G	G	G	G
189	A	A	A	A	A	A	A	A	A	A	A	A
190	A	A	A	A	A	A	A	A	A	A	A	A
191	G	G	G	G	G	G	A	A	A	A	A	A
192	A	A	A	A	A	A	A	A	A	A	A	A
193	A	A	A	A	A	A	A	A	A	A	A	A
194	A	A	A	A	A	A	A	A	A	A	A	A
195	G	G	G	G	G	G	C	C	C	C	C	C
196	C	C	C	C	C	C	C	C	C	C	C	C
197	A	A	A	A	A	A	A	A	A	A	A	A
198	C	C	C	C	C	C	A	A	A	A	A	A
199	G	G	G	G	G	G	T	T	T	T	T	T
200	T	T	T	T	T	T	T	T	T	T	T	T
201	C	C	C	C	C	C	T	T	T	T	T	T
202	C	C	C	C	C	C	T	T	T	T	T	T
203	T	T	T	T	T	T	T	T	T	T	T	T
204	C	C	C	C	C	C	T	T	T	T	T	T
205	T	T	T	T	T	T	G	G	G	G	G	G
206	G	G	G	G	G	G	C	C	C	C	C	C
207	C	C	C	C	C	C	T	T	T	T	T	T
208	T	T	T	T	T	T	T	T	T	T	T	T
209	T	T	T	T	T	T	T	T	T	T	T	T
210	C	C	C	C	C	C	T	T	T	T	T	T
211	T	T	T	T	T	T	C	C	C	C	C	C
212	C	C	C	C	C	C	A	A	A	A	A	A
213	A	A	A	A	A	A	A	A	A	A	A	A
214	A	A	A	A	A	A	A	A	A	A	A	A
215	A	A	A	A	A	A	A	A	A	A	A	A
216	A	A	A	A	A	A	A	A	A	A	A	A
217	A	A	A	A	A	A	A	A	A	A	A	A
218	A	A	A	A	A	A	A	A	A	A	A	A
219	A	A	A	A	A	A	A	A	A	A	A	A
220	A	A	A	A	A	A	A	A	A	A	A	A
221	C	C	C	C	C	C	C	C	C	C	C	C
222	T	T	T	T	T	T	G	G	G	G	G	G
223	G	G	G	G	G	G	A	A	A	A	A	A
224	A	A	A	A	A	A	A	A	A	A	A	A
225	G	G	G	G	G	G	A	A	A	A	A	A
226	A	A	A	A	A	A	G	G	G	G	G	G
227	T	T	T	T	T	T	G	G	G	G	G	G
228	G	G	G	G	G	G	G	G	G	G	G	G
229	C	C	C	C	C	C	A	A	A	A	A	A
230	A	A	A	A	A	A	A	A	A	A	A	A
231	A	A	A	A	A	A	A	A	A	A	A	A
232	A	A	A	A	A	A	A	A	A	A	A	A
233	C	C	C	C	C	C	C	C	C	C	C	C
234	C	C	C	C	C	C	C	C	C	C	C	C
235	G	G	G	G	G	G	G	G	G	G	G	G

Fig. 7.2 cont.

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Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Consensus of	Tm13 17	Consensus with	B1	Consensus with	AFP-3	Consensus with
236	A	A	A	A	A	A	A	A	A	A	C	N
237	A	A	A	A	A	A	A	A	A	A	C	N
238	G	C	C	G	G	G	T	N	T	N	C	N
239	C	C	C	C	C	C	C	C	C	C	G	C/G
240	C	C	C	C	C	C	G	G	G	G	G	N
241	G	G	G	G	G	G	G	G	G	G	G	G
242	A	A	A	A	A	A	A	A	A	A	G	A/T
243	G	A	A	A	A	A	A	A	A	A	A	A
244	A	A	A	A	A	A	A	A	A	A	A	A
245	A	A	A	A	A	A	A	A	A	A	A	A
246	C	C	C	C	C	C	A	C/G	A	A	A	A
247	A	A	A	A	A	A	G	R	A	A	A	A
248	C	C	C	C	C	C	T	Y	T	T	T	A
249	C	A	A	A	A	A	G	C/G	T	N	C	N
250	A	A	A	A	A	A	T	R	A	R	A	N
251	A	A	A	A	A	A	G	A/T	G	A	A	A
252	T	T	T	T	T	T	T	N	A	G	A	A
253	T	T	T	T	T	T	G	G	G	G	C	N
254	G	G	G	G	G	G	C	T	C	C	G	G/C
255	G	G	G	G	G	G	G	G	G	G	G	G
256	A	A	A	A	A	A	A	G/C	A	A	A	A
257	G	G	G	G	G	G	C	G	C	C	C	G/C
258	G	G	G	G	G	G	G	G/C	A	G/C	A	G/C
259	T	T	T	T	T	T	T	T	C	C	C	N
260	A	A	A	A	A	A	T	R	T	R	A	N
261	C	C	C	C	C	C	T	Y	T	Y	T	N
262	T	T	T	T	T	T	T	C/G	T	C	T	T
263	C	C	C	C	C	C	G	A	A	A	A	A
264	A	A	A	A	A	A	A	R	A	R	A	A
265	A	A	A	A	A	A	G	R	A	R	A	A
266	A	A	A	A	A	A	G	R	A	R	A	A
267	G	G	G	G	G	G	C	N	G	G	C	R
268	C	C	C	C	C	C	A	C/G	A	C/G	A	C/G
269	C	C	C	C	C	C	A	A	A	A	A	A
270	A	A	A	A	A	A	G	G	T	G	A	A
271	A	A	A	A	A	A	T	A	A	A	A	A
272	G	G	G	G	G	G	G	C/G	G	G	T	N
273	C	C	C	C	C	C	T	T	T	T	T	T
274	T	T	T	T	T	T	G	T	T	T	T	T
275	T	T	T	T	T	T	A	A	A	A	A	A
276	A	A	A	A	A	A	A	R	A	A	A	A
277	A	A	A	A	A	A	A	G	A	A	A	A
278	G	G	G	G	G	G	G	N	A	A	A	A
279	C	C	C	C	C	C	A	A	G	A	A	A
280	A	A	A	A	A	A	G	N	A	A	A	A
281	T	T	T	T	T	T	T	A	G	A	A	A
282	T	T	T	T	T	T	G	T	T	T	A	A
283	G	G	G	G	G	G	C	T	A	C	C	A
284	G	G	G	G	G	G	A	G/C	R	C	T	N
285	C	C	C	C	C	C	C	R	A	A	C	N
286	C	C	C	C	C	C	A	C	A	A	T	N
287	C	C	C	C	C	C	T	C	A	A	G	N
288	C	C	C	C	C	C	G	R	A	A	A	N
289	A	A	A	A	A	A	A	R	A	A	A	A
290	C	C	C	C	C	C	A	R	A	A	A	A
291	C	C	C	C	C	C	A	R	A	A	A	A
292							A	C	A	A	A	A
293							A	C	A	A	A	A
294							A	C	A	A	A	A
295	G	G	G	G	G	G	A	C	A	A	A	A
296	A	A	A	A	A	A	A	C	A	A	A	A
297	C	C	C	C	C	C	A	C	A	A	A	A
298	G	G	G	G	G	G	A	G	A	A	A	A
299	A	A	A	A	A	A	A	A	A	A	A	A
300	A	A	A	A	A	A	A	A	A	A	A	A
301	A	A	A	A	A	A	A	A	A	A	A	A
302	G	G	G	G	G	G	A	A	A	A	A	A
303	T	T	T	T	T	T	A	A	A	A	A	A
304	G	G	G	G	G	G	A	A	A	A	A	A
305	T	T	T	T	T	T	A	A	A	A	A	A
306	G	G	G	G	G	G	A	A	A	A	A	A
307	A	A	A	A	A	A	A	A	A	A	A	A
308	C	C	C	C	C	C	A	A	A	A	A	A
309	A	A	A	A	A	A	A	A	A	A	A	A
310	A	A	A	A	A	A	A	A	A	A	A	A
311	A	A	A	A	A	A	A	A	A	A	A	A
312	T	T	T	T	T	T	A	A	A	A	A	A
313	C	C	C	C	C	C	A	A	A	A	A	A
314	T	T	T	T	T	T	A	A	A	A	A	A
315	C	C	C	C	C	C	A	A	A	A	A	A
316	T	T	T	T	T	T	A	A	A	A	A	A
317	G	G	G	G	G	G	A	A	A	A	A	A
318	C	C	C	C	C	C	A	A	A	A	A	A
319	A	A	A	A	A	A	A	A	A	A	A	A
320	G	G	G	G	G	G	A	A	A	A	A	A
321	A	A	A	A	A	A	A	A	A	A	A	A
322	A	A	A	A	A	A	A	A	A	A	A	A
323	G	G	G	G	G	G	A	A	A	A	A	A
324	T	T	T	T	T	T	A	A	A	A	A	A
325	G	G	G	G	G	G	A	A	A	A	A	A
326	C	C	C	C	C	C	A	A	A	A	A	A
327	T	T	T	T	T	T	A	A	A	A	A	A
328	G	G	G	G	G	G	A	A	A	A	A	A
329	T	T	T	T	T	T	A	A	A	A	A	A
330	G	G	G	G	G	G	A	A	A	A	A	A
331	T	T	T	T	T	T	A	A	A	A	A	A
332	C	C	C	C	C	C	A	A	A	A	A	A
333	A	A	A	A	A	A	A	A	A	A	A	A
334	A	A	A	A	A	A	A	A	A	A	A	A
335	G	G	G	G	G	G	A	A	A	A	A	A
336	A	A	A	A	A	A	A	A	A	A	A	A
337	A	A	A	A	A	A	A	A	A	A	A	A
338	G	G	G	G	G	G	A	A	A	A	A	A
339	G	G	G	G	G	G	A	A	A	A	A	A
340	C	C	C	C	C	C	A	A	A	A	A	A
341	C	C	C	C	C	C	A	A	A	A	A	A
342	C	C	C	C	C	C	A	A	A	A	A	A
343	A	A	A	A	A	A	A	A	A	A	A	A
344	C	C	C	C	C	C	A	A	A	A	A	A
345	A	A	A	A	A	A	A	A	A	A	A	A
346	C	C	C	C	C	C	A	A	A	A	A	A
347	A	A	A	A	A	A	A	A	A	A	A	A
348	G	G	G	G	G	G	A	A	A	A	A	A
349	A	A	A	A	A	A	A	A	A	A	A	A
350	A	A	A	A	A	A	A	A	A	A	A	A
351	A	A	A	A	A	A	A	A	A	A	A	A
352	A	A	A	A	A	A	A	A	A	A	A	A
353	A	A	A	A	A	A	A	A	A	A	A	A

Fig. 7.2 cont.

Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Consensus of	Tm13 17	Consensus with	B1	Consensus with	AFP-3	Consensus with
354	A	A	A	A	A	A	G	R	A	R	C	N
355	A	A	A	A	A	A	A	A	C	N	T	N
356	C	G	G	G	G	G	G	G	C	C	C	C
357	G	G	G	G	G	G	G	G	C	C	C	C
358	C	C	C	C	C	C	C	C	A	A	T	N
359	T	T	T	T	T	T	T	T	T	T	C	N
360	A	A	A	A	A	A	A	A	A	A	C	N
361	T	T	T	T	T	T	T	T	G	G	C	N
362	A	A	A	A	A	A	A	A	A	A	C	N
363	G	G	G	G	G	G	A	A	A	A	C	N
364	A	A	A	A	A	A	A	A	G	G	A	N
365	C	C	C	C	C	C	A	A	A	A	C	N
366	A	A	A	A	A	A	A	A	G	G	A	N
367	C	C	C	C	C	C	A	A	T	T	T	A
368	C	C	C	C	C	C	A	A	T	T	T	A
369	T	T	T	T	T	T	T	T	A	A	T	N
370	T	T	T	T	T	T	T	T	C	C	T	N
371	T	T	T	T	T	T	T	T	A	A	T	N
372	C	C	C	C	C	C	A	A	A	A	T	N
373	A	A	A	A	A	A	A	A	A	A	A	N
374	A	A	A	A	A	A	A	A	A	A	A	N
375	G	G	G	G	G	G	A	A	A	A	G	N
376	T	T	T	T	T	T	G	G	T	T	T	N
377	A	A	A	A	A	A	T	T	T	T	T	N
378	T	T	T	T	T	T	C	C	A	A	T	N
379	A	A	A	A	A	A	T	T	G	G	T	N
380	T	T	T	T	T	T	T	T	A	A	T	N
381	T	T	T	T	T	T	T	T	T	T	T	N
382	A	A	A	A	A	A	T	T	T	T	T	N
383	C	C	C	C	C	C	G	G	A	A	C	N
384	G	G	G	G	G	G	A	A	G	G	A	N
385	A	A	A	A	A	A	A	A	A	A	T	N
386	C	C	C	C	C	C	A	A	A	A	C	N
387	A	A	A	A	A	A	A	A	A	A	C	N
388	C	C	C	C	C	C	A	A	A	A	C	N
389	A	A	A	A	A	A	A	A	A	A	C	N
390	A	A	A	A	A	A	A	A	A	A	C	N
391	A	A	A	A	A	A	A	A	A	A	C	N
392	A	A	A	A	A	A	A	A	A	A	C	N
393	A	A	A	A	A	A	A	A	A	A	C	N
394	C	C	C	C	C	C	C	C	C	C	C	N
395	C	C	C	C	C	C	C	C	C	C	C	N
396	C	C	C	C	C	C	C	C	C	C	C	N
397	C	C	C	C	C	C	C	C	C	C	C	N
398	C	C	C	C	C	C	C	C	C	C	C	N
399	C	C	C	C	C	C	C	C	C	C	C	N
400	G	G	G	G	G	G	A	A	A	A	T	N
401	A	A	A	A	A	A	A	A	A	A	T	N
402	T	T	T	T	T	T	C	C	T	T	T	N
403	C	C	C	C	C	C	C	C	T	T	T	N
404	T	T	T	T	T	T	C	C	T	T	T	N
405	C	C	C	C	C	C	C	C	T	T	T	N
406	C	C	C	C	C	C	C	C	T	T	T	N
407	C	C	C	C	C	C	C	C	T	T	T	N
408	A	A	A	A	A	A	A	A	G	G	A	N
409	T	T	T	T	T	T	A	A	A	A	T	N
410	A	A	A	A	A	A	A	A	A	A	T	N
411	T	T	T	T	T	T	A	A	A	A	T	N
412	G	G	G	G	G	G	T	T	T	T	T	N
413	A	A	A	A	A	A	T	T	T	T	T	N
414	T	T	T	T	T	T	T	T	T	T	T	N
415	A	A	A	A	A	A	T	T	T	T	T	N
416	T	T	T	T	T	T	T	T	T	T	T	N
417	T	T	T	T	T	T	T	T	T	T	T	N
418	A	A	A	A	A	A	T	T	T	T	T	N
419	T	T	T	T	T	T	T	T	T	T	T	N
420	T	T	T	T	T	T	T	T	T	T	T	N
421	T	T	T	T	T	T	T	T	T	T	T	N
422	T	T	T	T	T	T	T	T	T	T	T	N
423	T	T	T	T	T	T	T	T	T	T	T	N
424	T	T	T	T	T	T	T	T	T	T	T	N
425	T	T	T	T	T	T	T	T	T	T	T	N
426	T	T	T	T	T	T	T	T	T	T	T	N
427	T	T	T	T	T	T	T	T	T	T	T	N
428	T	T	T	T	T	T	T	T	T	T	T	N
429	A	A	A	A	A	A	A	A	A	A	T	N
430	T	T	T	T	T	T	A	A	A	A	T	N
431	T	T	T	T	T	T	A	A	A	A	T	N
432	T	T	T	T	T	T	A	A	A	A	T	N
433	G	G	G	G	G	G	A	A	A	A	T	N
434	A	A	A	A	A	A	A	A	A	A	T	N
435	C	C	C	C	C	C	A	A	A	A	T	N
436	T	T	T	T	T	T	A	A	A	A	T	N
437	G	G	G	G	G	G	A	A	A	A	T	N
438	A	A	A	A	A	A	A	A	A	A	T	N
439	A	A	A	A	A	A	A	A	A	A	T	N
440	T	T	T	T	T	T	A	A	A	A	T	N
441	T	T	T	T	T	T	A	A	A	A	T	N
442	T	T	T	T	T	T	A	A	A	A	T	N
443	T	T	T	T	T	T	A	A	A	A	T	N
444	T	T	T	T	T	T	A	A	A	A	T	N
445	G	G	G	G	G	G	A	A	A	A	T	N
446	A	A	A	A	A	A	A	A	A	A	T	N
447	A	A	A	A	A	A	A	A	A	A	T	N
448	A	A	A	A	A	A	A	A	A	A	T	N
449	A	A	A	A	A	A	A	A	A	A	T	N
450	A	A	A	A	A	A	A	A	A	A	T	N
451	A	A	A	A	A	A	A	A	A	A	T	N
452	A	A	A	A	A	A	A	A	A	A	T	N
453	A	A	A	A	A	A	A	A	A	A	T	N
454	A	A	A	A	A	A	A	A	A	A	T	N
455	A	A	A	A	A	A	A	A	A	A	T	N
456	A	A	A	A	A	A	A	A	A	A	T	N
457	A	A	A	A	A	A	A	A	A	A	T	N
458	A	A	A	A	A	A	A	A	A	A	T	N
459	A	A	A	A	A	A	A	A	A	A	T	N
460	A	A	A	A	A	A	A	A	A	A	T	N
461	A	A	A	A	A	A	A	A	A	A	T	N
462	A	A	A	A	A	A	A	A	A	A	T	N
463	A	A	A	A	A	A	A	A	A	A	T	N
464	A	A	A	A	A	A	A	A	A	A	T	N
465	A	A	A	A	A	A	A	A	A	A	T	N
466	A	A	A	A	A	A	A	A	A	A	T	N
467	A	A	A	A	A	A	A	A	A	A	T	N
468	A	A	A	A	A	A	A	A	A	A	T	N
469	A	A	A	A	A	A	A	A	A	A	T	N
470	A	A	A	A	A	A	A	A	A	A	T	N
471	A	A	A	A	A	A	A	A	A	A	T	N

Fig. 7.2 cont.

Position	Tm12 84-2.2	Tm12 84-2.3	Tm12 84-3.4	Tm12 84-3.9	Tm12 84-7.5	Consensus of	Tm13 17	Consensus with	B1	Consensus with	AFP-3	Consensus with
472	A	A	A	A	A	A	A	A		A	A	A
473	A	A	A	A	A	A	A	A		A	A	A
474	T	T	T	T	T	T	T	T		T	T	T
475	A	A	A	A	A	A	A	A		A	A	A
476	A	A	A	A	A	A	A	A		A	A	A
477	A	A	A	A	A	A	A	A		A	A	A
478	G	G	G	G	G	G	G	G		G	A	N
479	G	G	G	G	G	G	G	G		N	T	N
480	T	T	T	T	T	T	T	T		N	T	N
481	A	A	A	A	A	A	A	A		N	T	N
482	A	C	C	C	C	C	T	Y		Y	A	N
483	T	T	T	T	T	T	T	T		T	A	A/T
484	A	T	T	T	T	T	C	N		N	G	A/T
485	T	C	C	C	C	C	T	T		T	A	N
486	C	G	G	G	G	G	G	R		N	A	R
487	G	G	G	G	G	G	A	R		R	A	T/A
488	Y	T	T	T	T	T	T	T		T	A	N
489	I	T	T	T	T	T	G	N		N	A	N
490	A	T	T	T	T	T	A	N		N	A	R
491	T	T	T	T	T	T	T	N		N	A	N
492	G	G	G	G	G	G	A	R		R	A	N
493	T	A	A	A	A	A	A	N		N	A	N
494	A	A	A	A	A	A	A	A		A	A	A
495	A	A	A	A	A	A	A	A		A	A	A
496	A	A	A	A	A	A	A	A		A	A	A
497	A	A	A	A	A	A	A	A		A	A	A
498	A	A	A	A	A	A	A	A		A	A	A
499	A	A	A	A	A	A	A	A		A	A	A
500	A	A	A	A	A	A	A	A		A	A	A
501	A	A	A	A	A	A	A	A		A	A	A
502	A	A	A	A	A	A	A	A		A	A	A
503	A	A	A	A	A	A	A	A		A	A	A
504	A	A	A	A	A	A	A	A		A	A	A
505	A	A	A	A	A	A	A	A		A	A	A
506	A	A	A	A	A	A	A	A		A	A	A
507	A	A	A	A	A	A	A	A		A	A	A
508	A	A	A	A	A	A	A	A		A	A	A
509	A	A	A	A	A	A	A	A		A	A	A
510	A	A	A	A	A	A	A	A		A	A	A
511	A	A	A	A	A	A	A	A		A	A	A
512												

Fig. 7.2 cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus Tm 12.84	Tm P-B1	Tm P-B2	Consensus to Tm13.17	Tm AFP-3	Consensus to AFP-3	GENERAL CONSENSUS	SUBSTITUTIONS - most to least common
1	M	M	M	M	M	M	L	L	HY, ALP/SUL	M	M	K	
2	K	K	K	K	K	K	T	T	M	K	M	K	
3	L	L	L	L	L	L	S	S	K	L	K	L	
4	L	L	L	L	L	L	T	T	L	L	L	L	
5	L	L	L	L	L	L	T	T	L	L	L	L	
6	L	L	L	L	L	L	T	T	L	L	L	L	
7	L	L	L	L	L	L	T	T	L	L	L	L	
8	L	L	L	L	L	L	T	T	L	L	L	L	
9	L	L	L	L	L	L	T	T	L	L	L	L	
10	L	L	L	L	L	L	T	T	L	L	L	L	
11	L	L	L	L	L	L	T	T	L	L	L	L	
12	L	L	L	L	L	L	T	T	L	L	L	L	
13	L	L	L	L	L	L	T	T	L	L	L	L	
14	L	L	L	L	L	L	T	T	L	L	L	L	
15	L	L	L	L	L	L	T	T	L	L	L	L	
16	L	L	L	L	L	L	T	T	L	L	L	L	
17	L	L	L	L	L	L	T	T	L	L	L	L	
18	L	L	L	L	L	L	T	T	L	L	L	L	
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20	L	L	L	L	L	L	T	T	L	L	L	L	
21	L	L	L	L	L	L	T	T	L	L	L	L	
22	L	L	L	L	L	L	T	T	L	L	L	L	
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76	L	L	L	L	L	L	T	T	L	L	L	L	
77	L	L	L	L	L	L	T	T	L	L	L	L	
78	L	L	L	L	L	L	T	T	L	L	L	L	

Fig. 7.3

00076793 004202

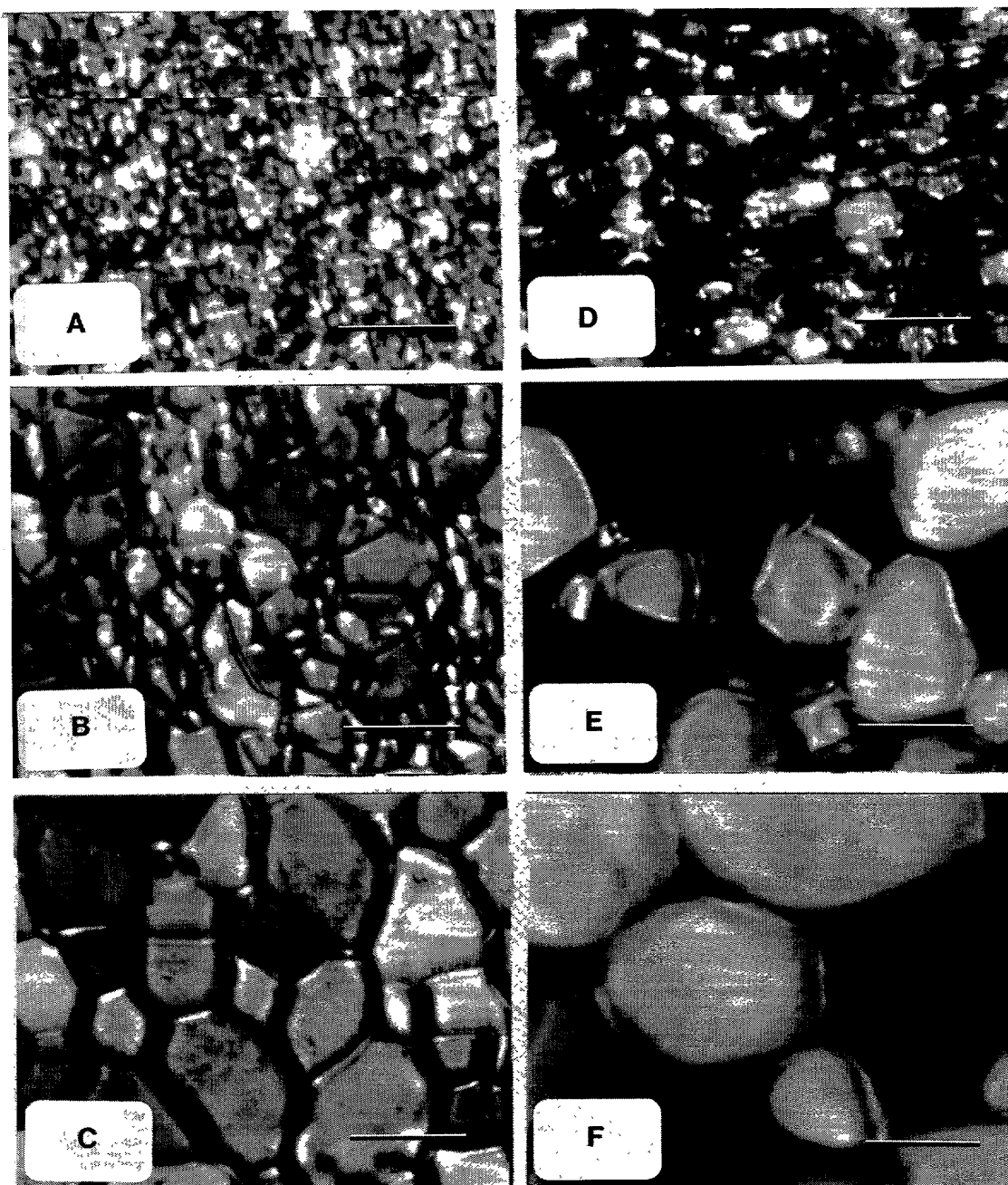


Fig. 8.0

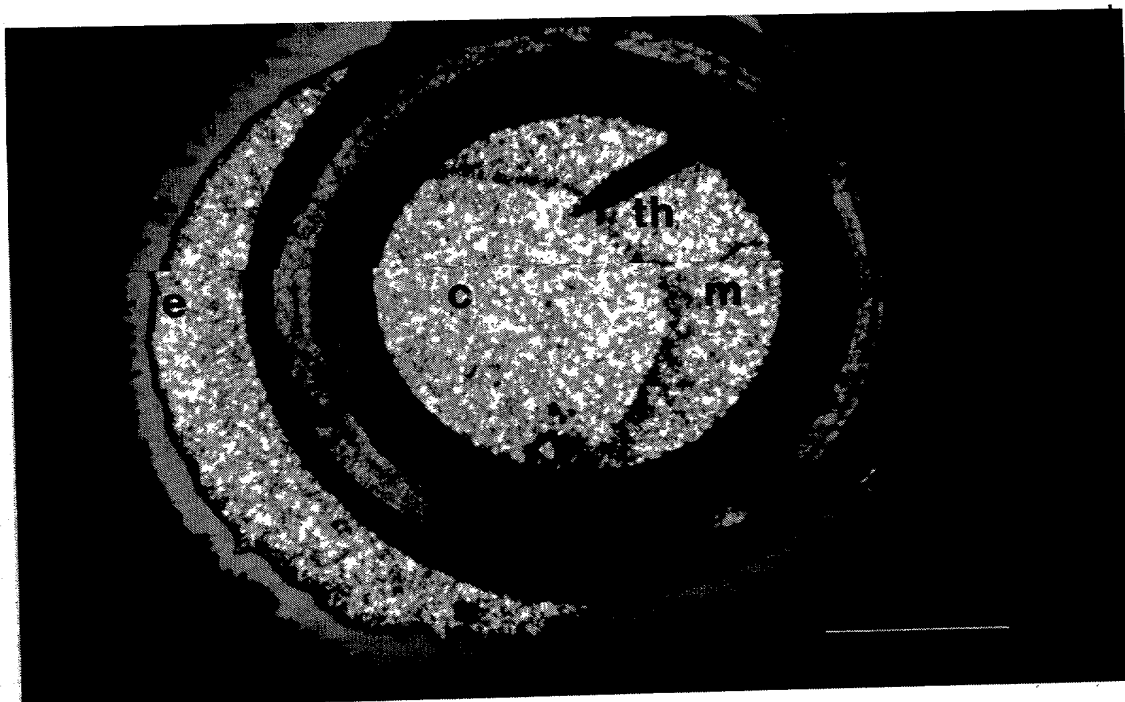


Fig. 8.1a

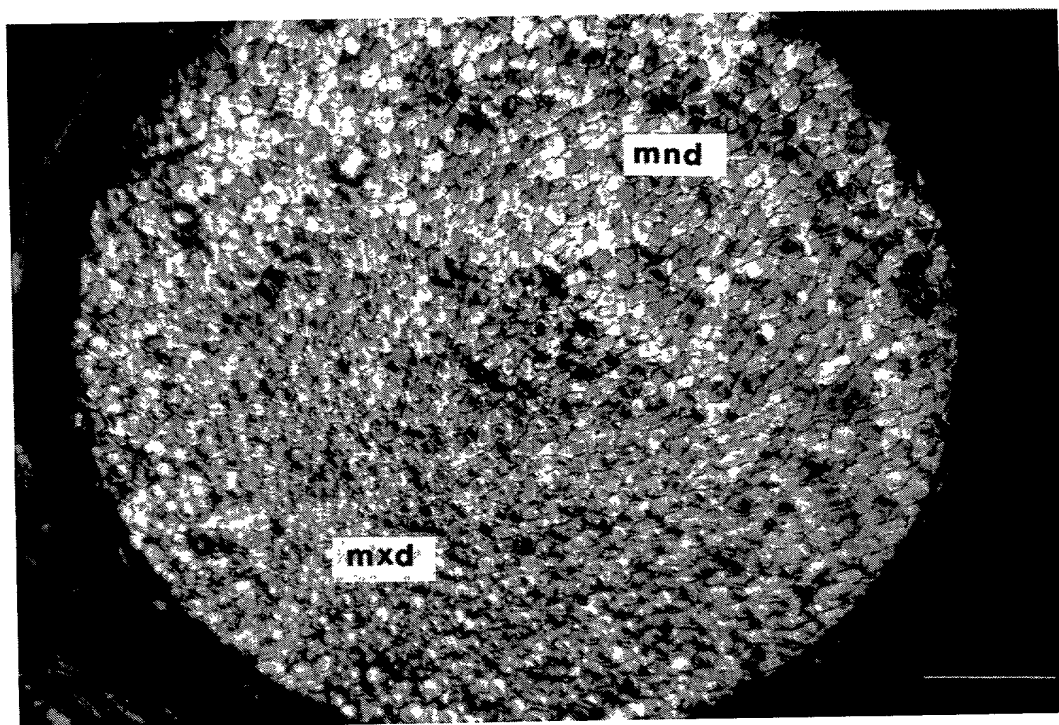
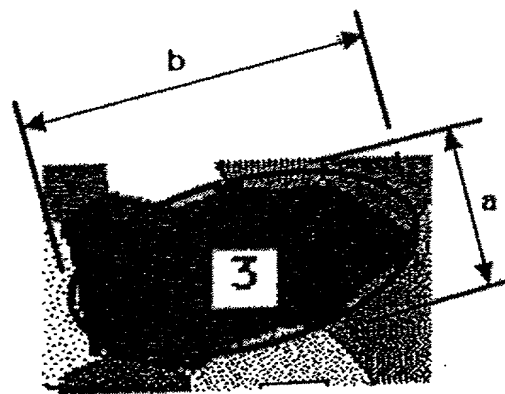


Fig. 8.1b

202500"06404060



grain area=0.25 μ b

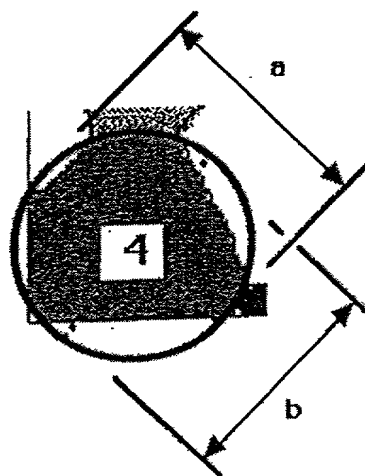
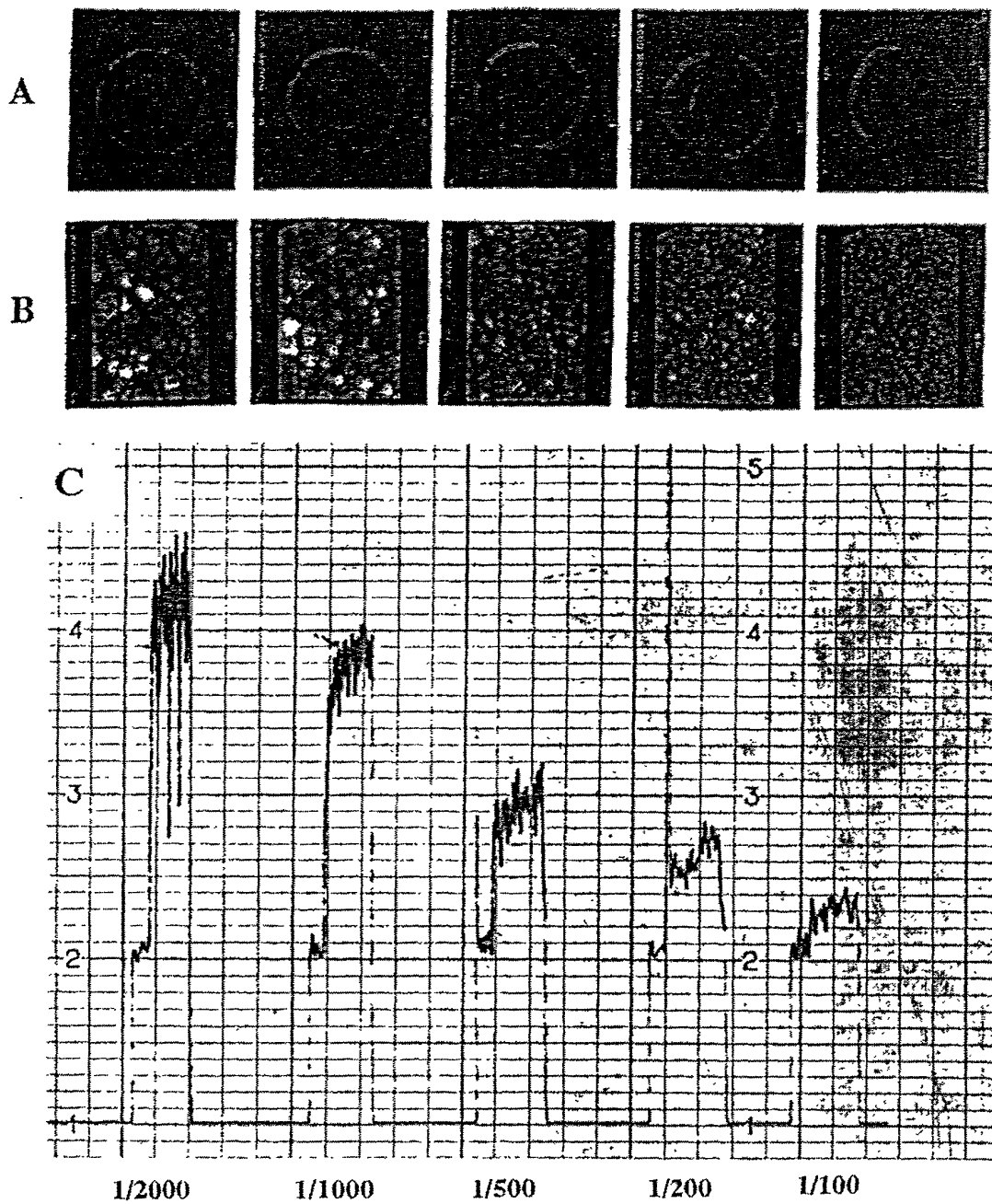


Fig. 8.2

*Fig. 8.3*

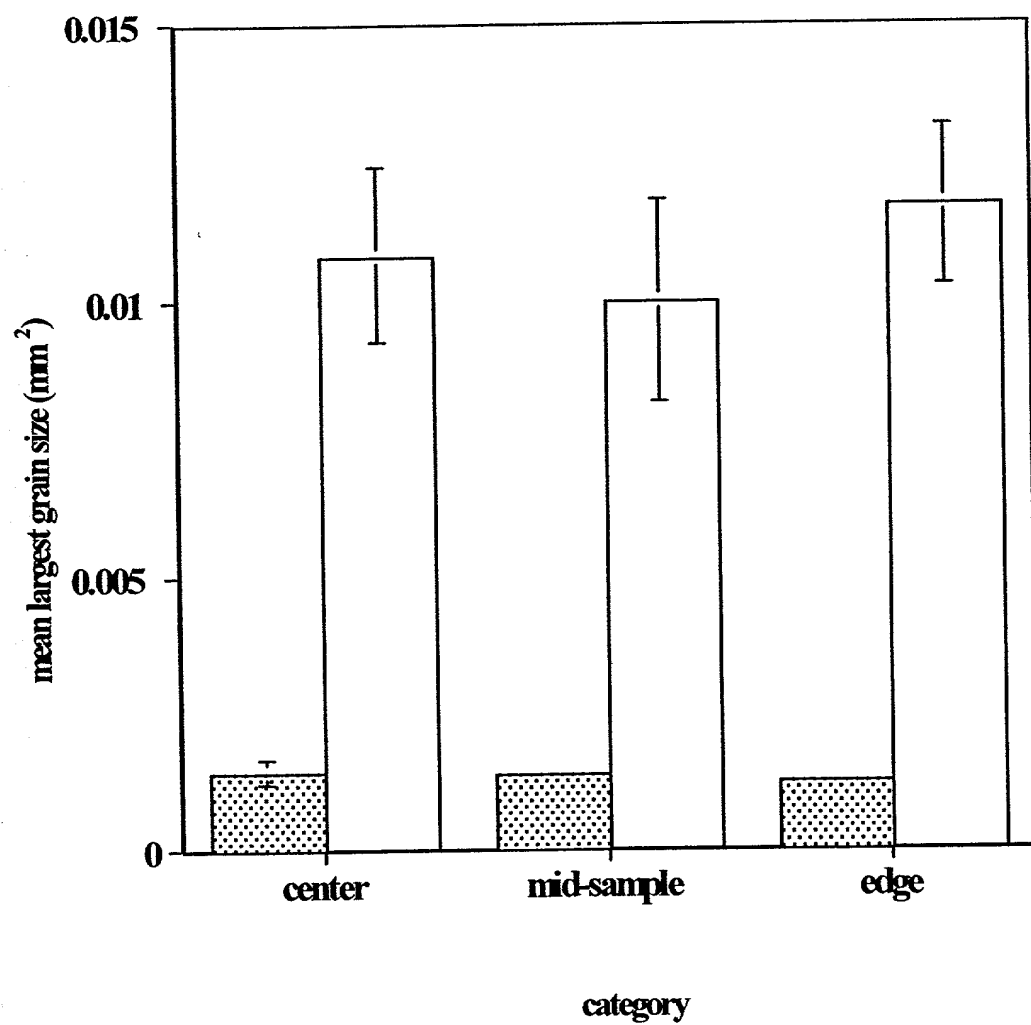


Fig. 8.4a

202120 35434350

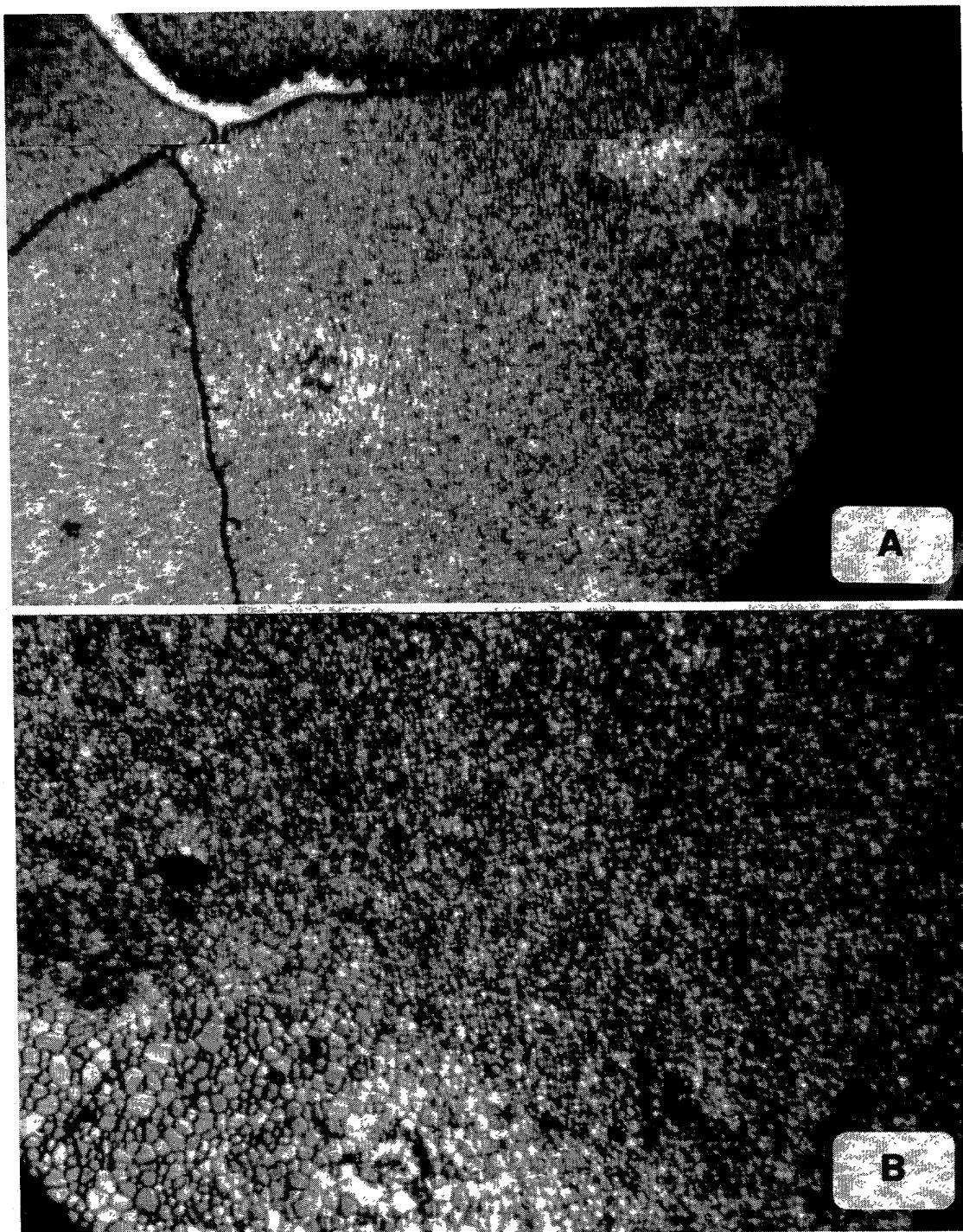


Fig. 8.4b

2025-11-23 15:42:00

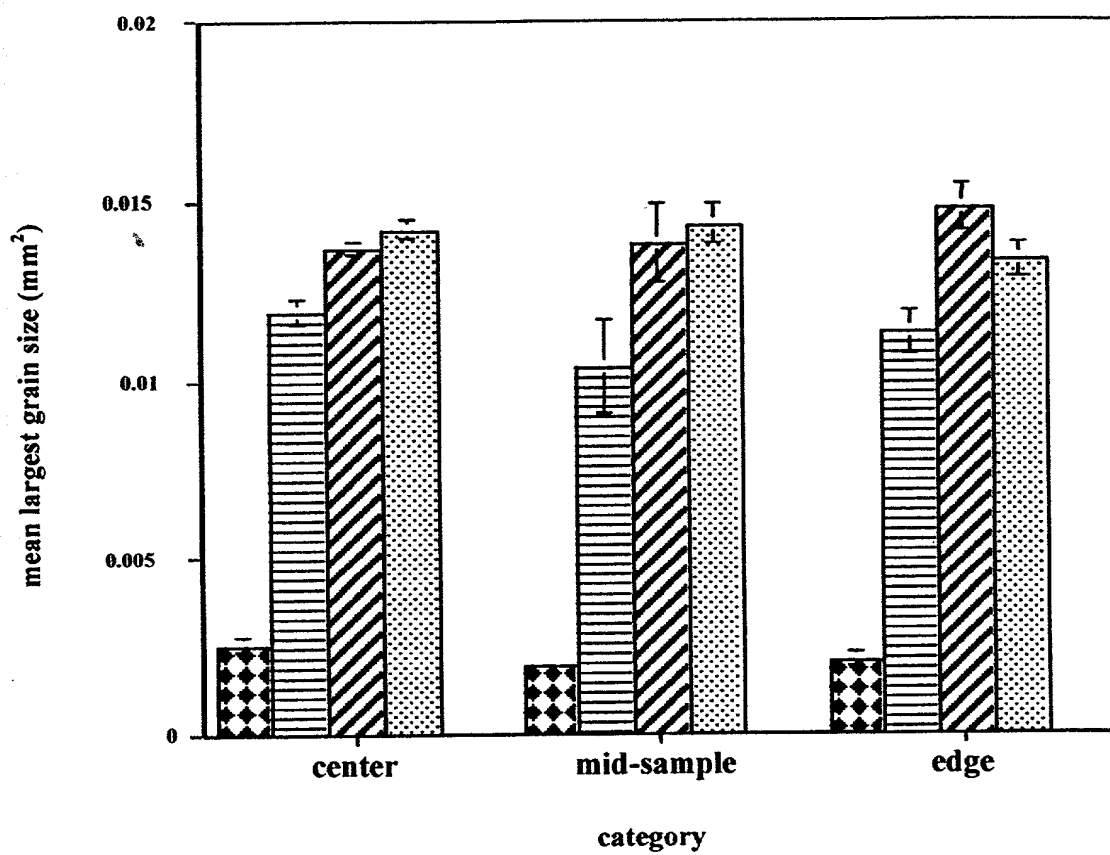


Fig. 8.5a

A high-contrast, black and white photograph of a circular, textured object, possibly a lens or a coin, centered against a dark background. The object has concentric rings and a grainy surface.

Fig. 8.5b

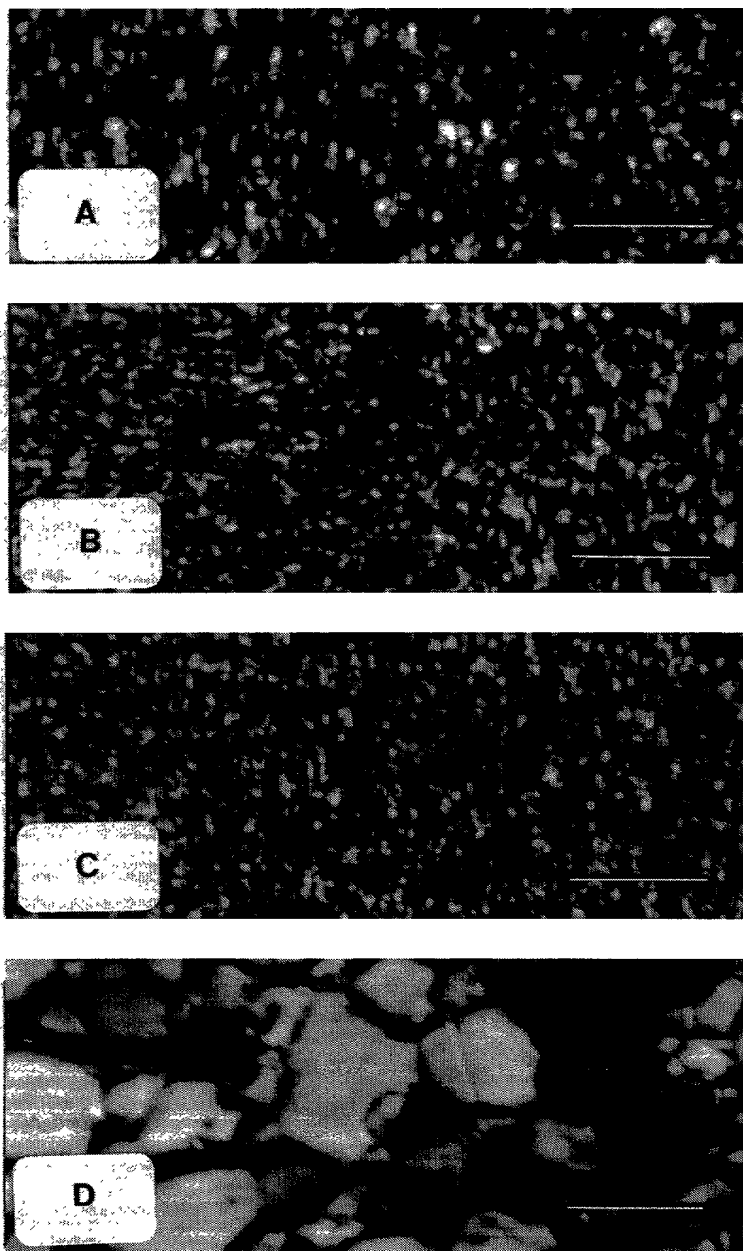


Fig. 8.6

Fig. 8.7

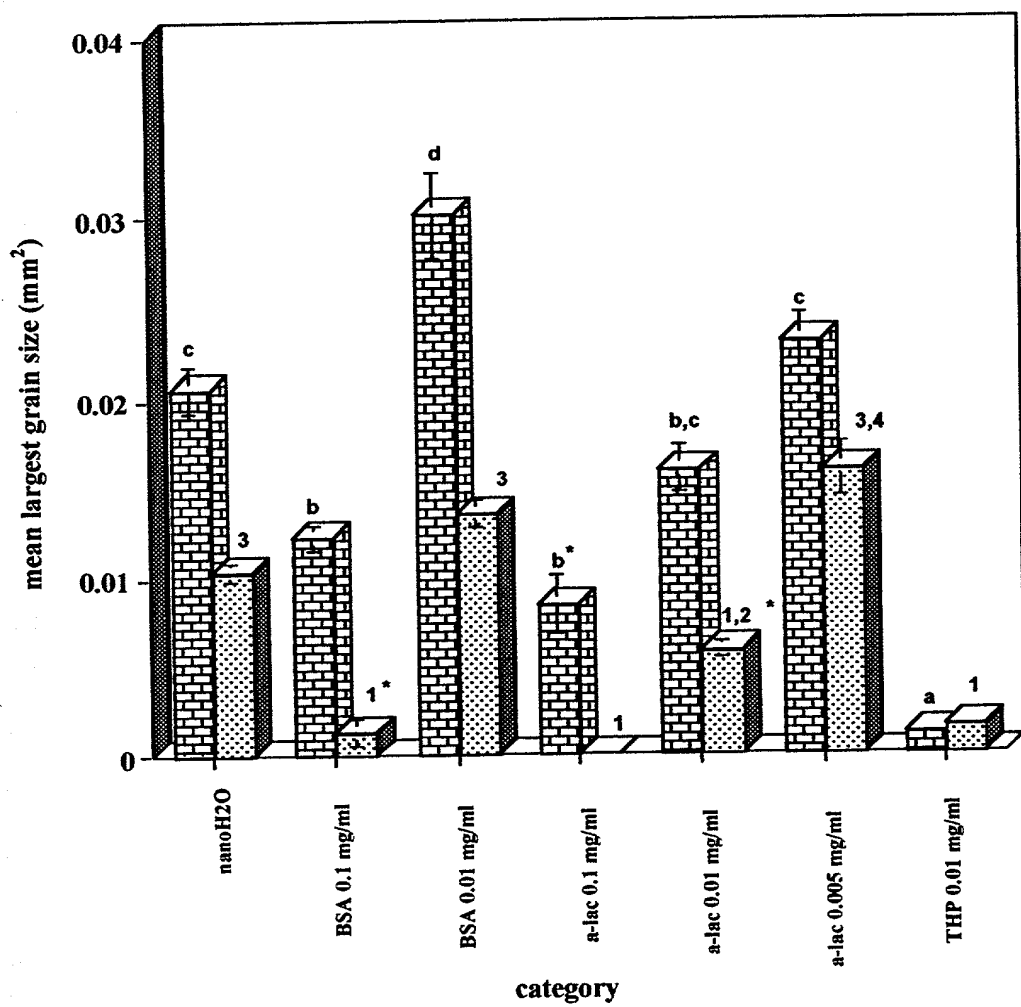


Fig. 8.8

202303062000

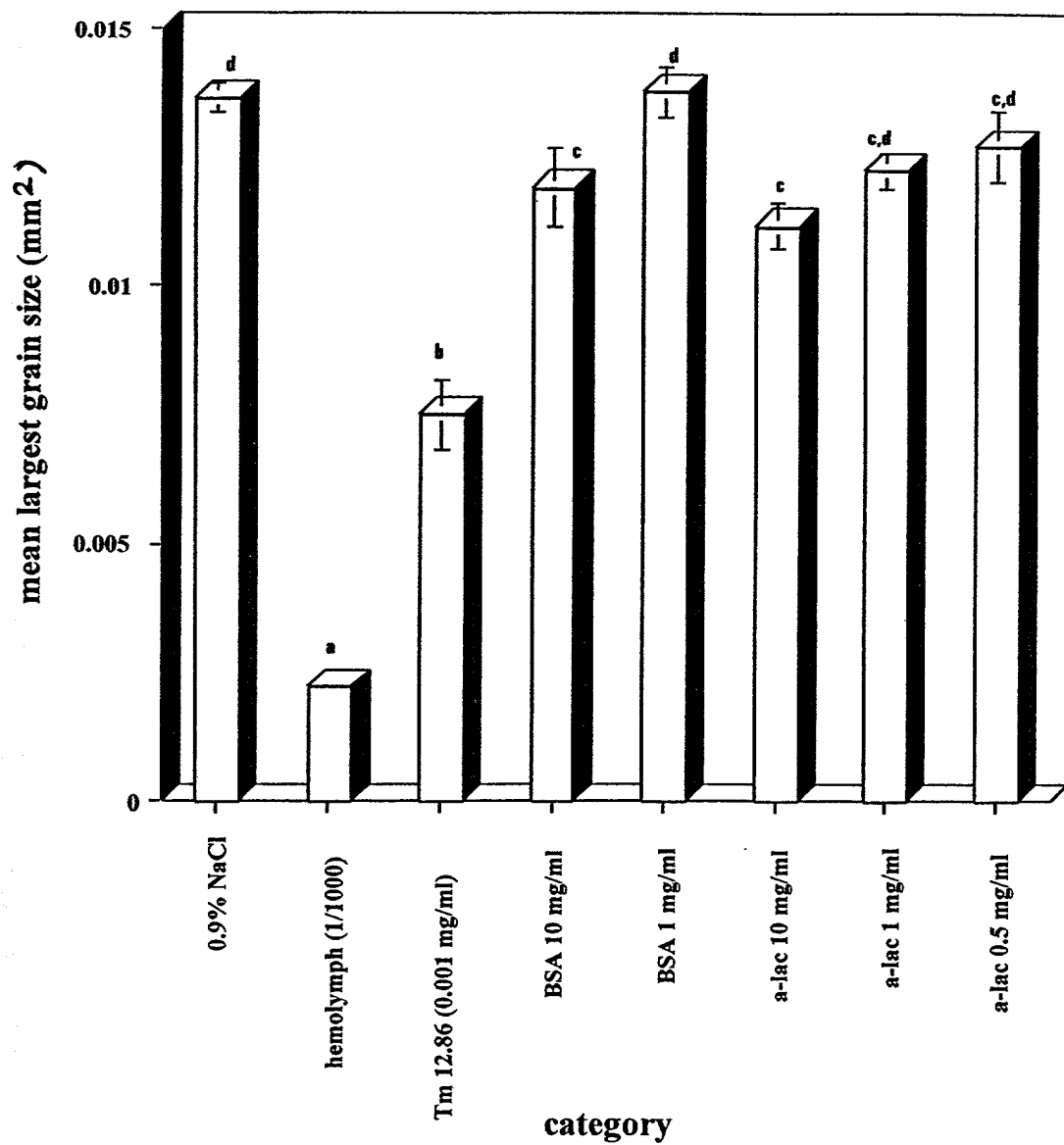


Fig. 8.9

2025-06-29 09:00

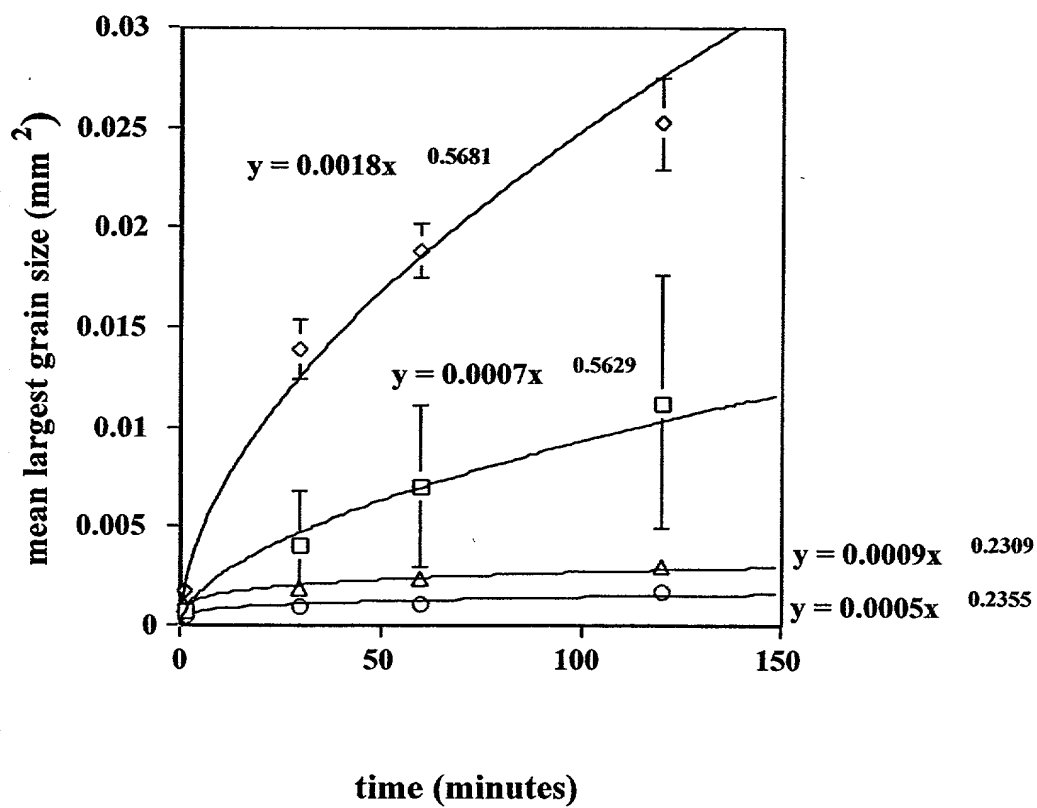


Fig. 8.10

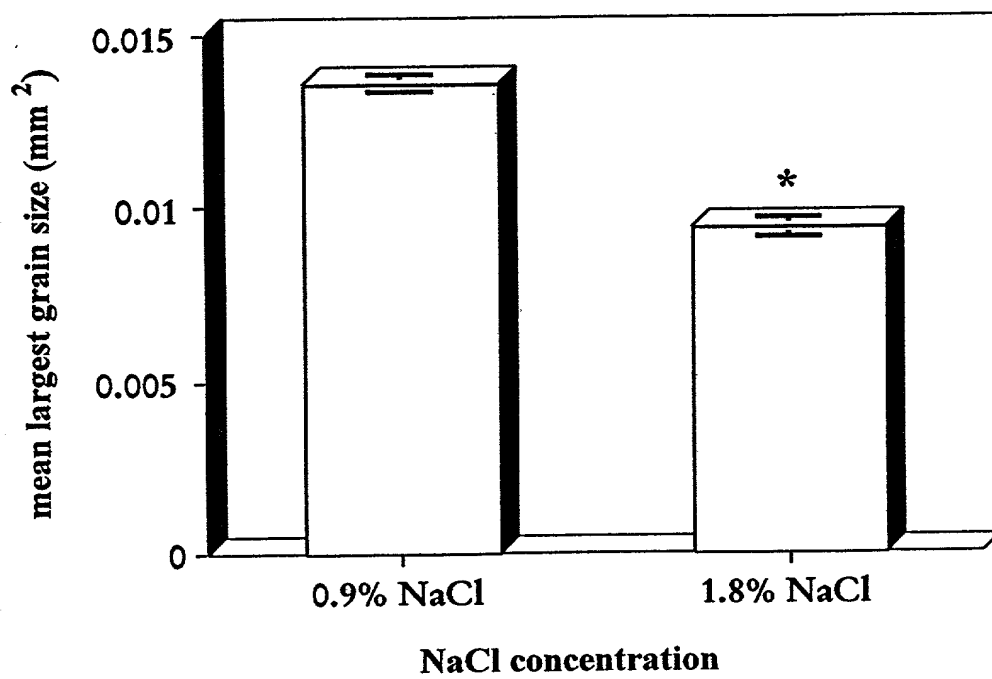


Fig. 8.11

202509260950

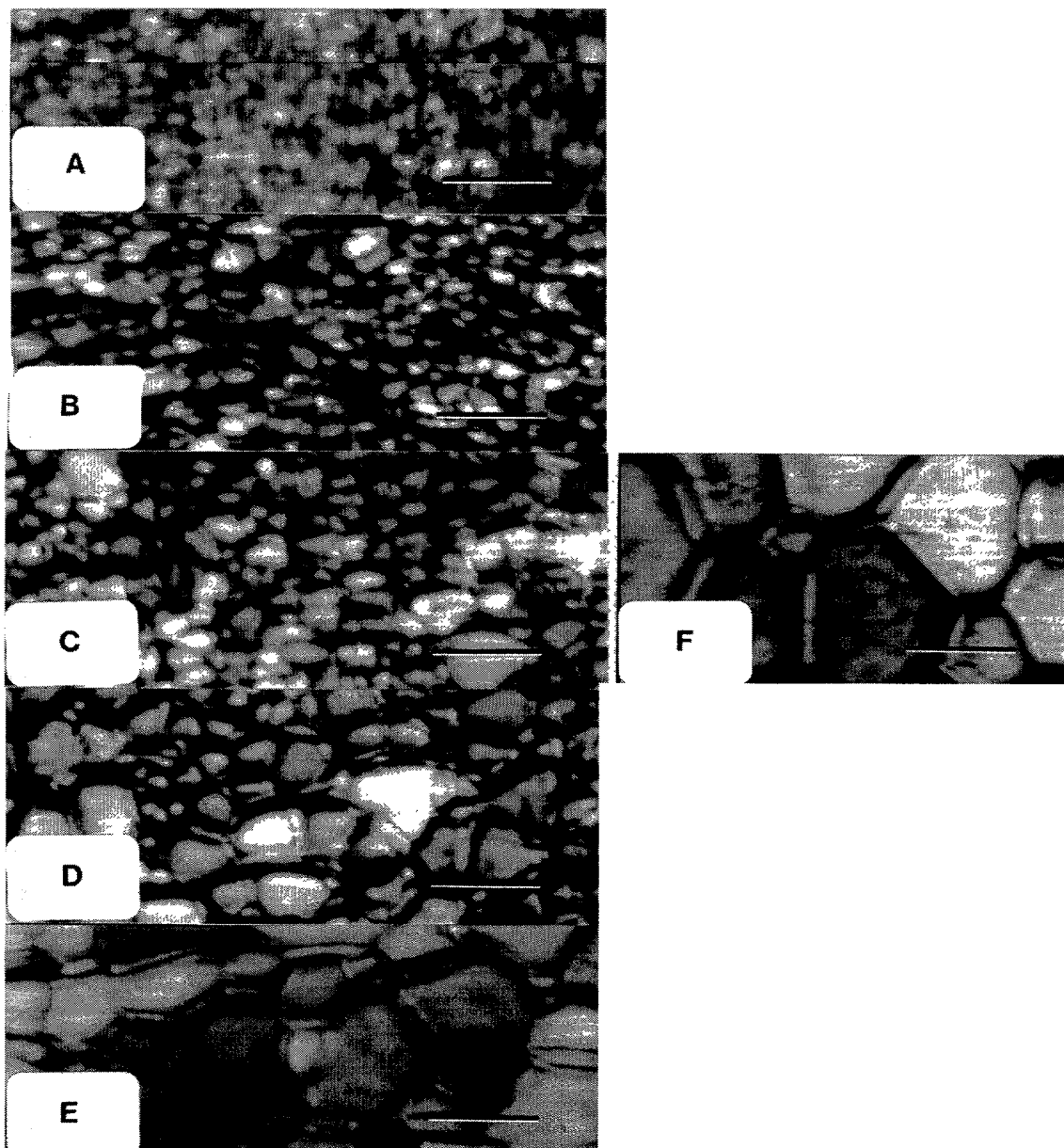


Fig. 8.12

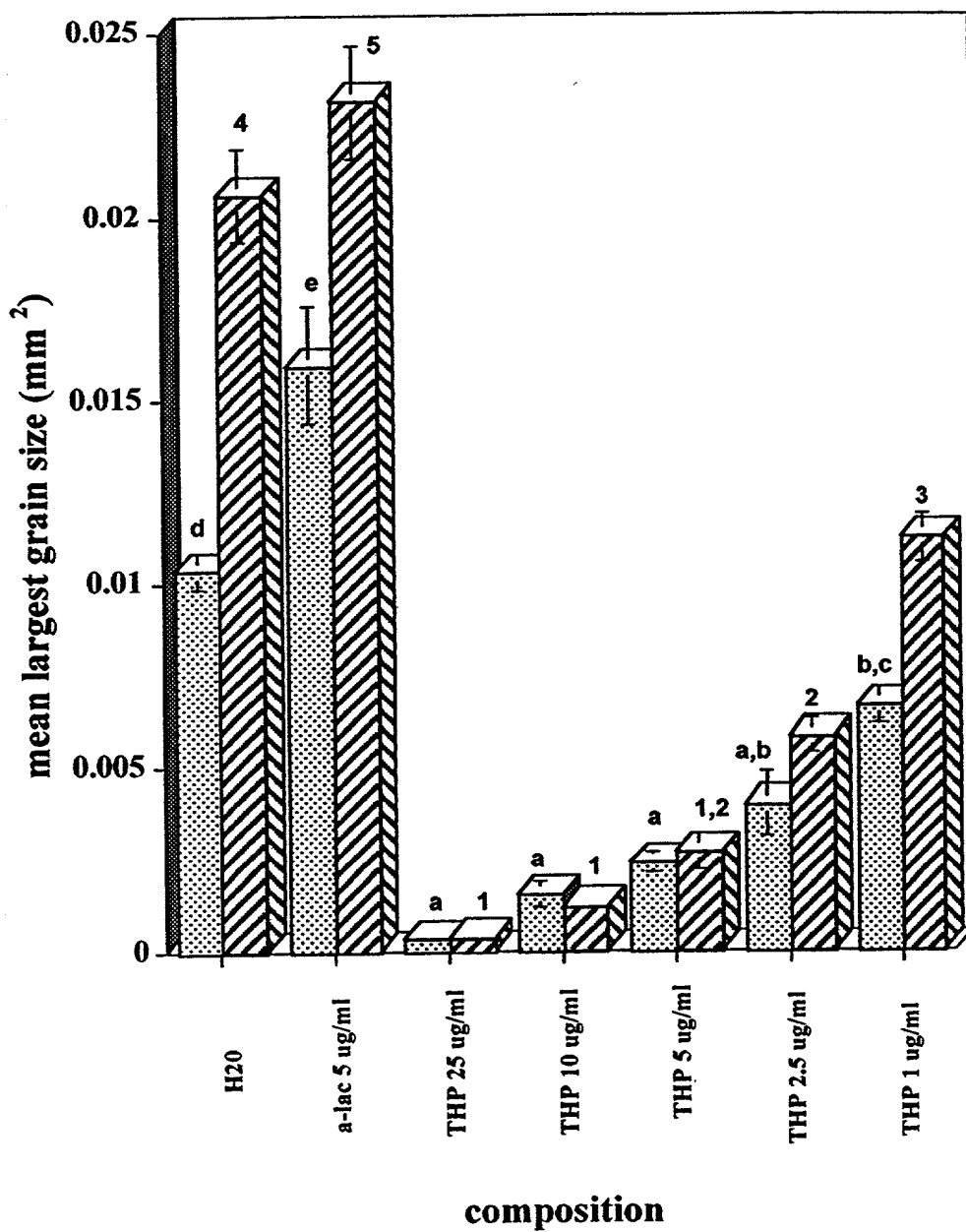


Fig. 8.13

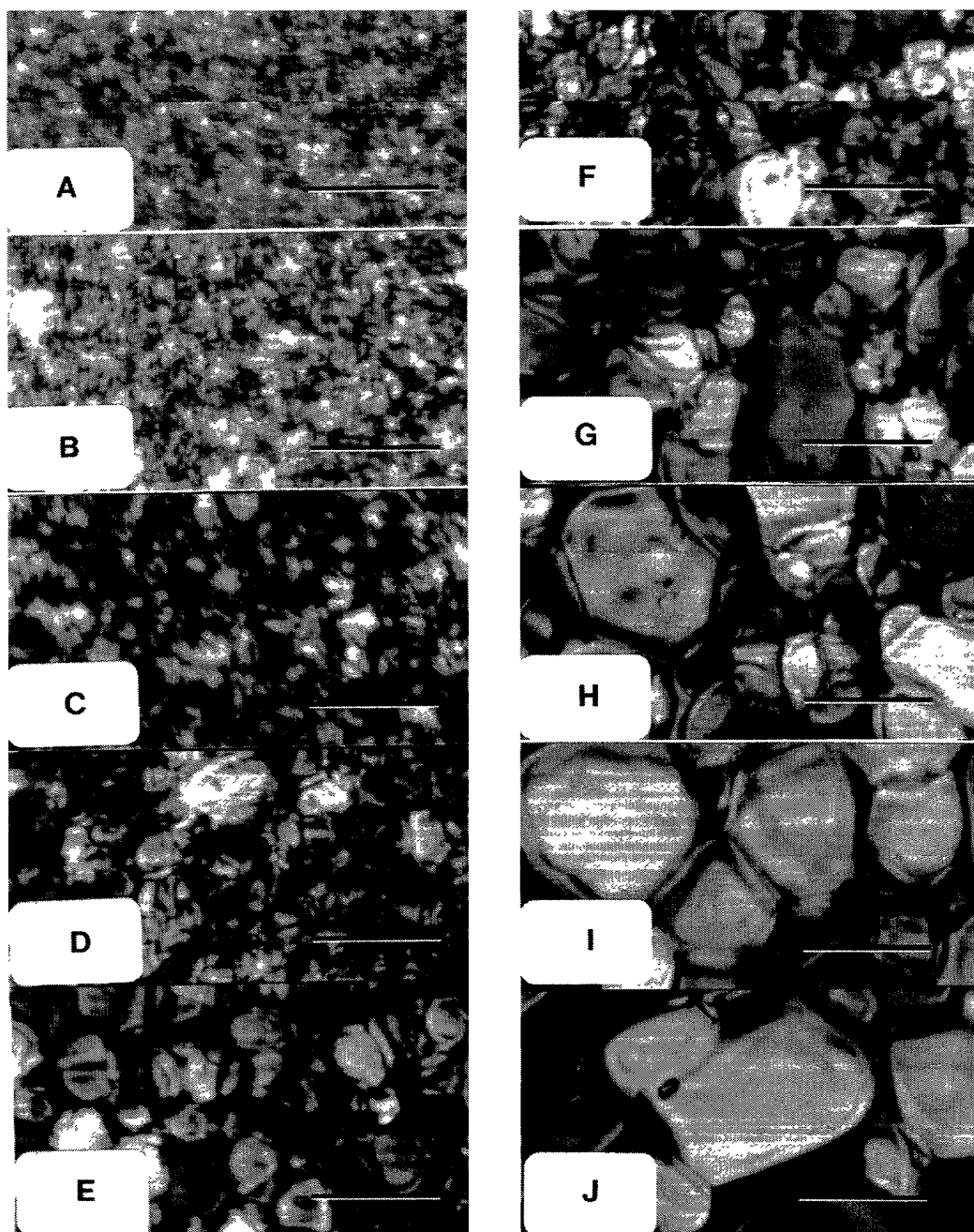


Fig. 8.14

Fig. 8.15

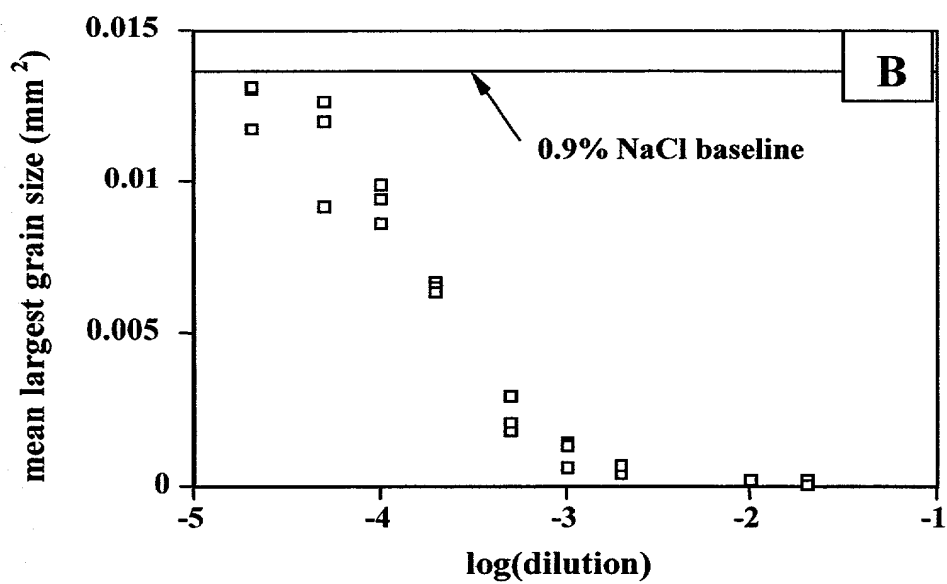
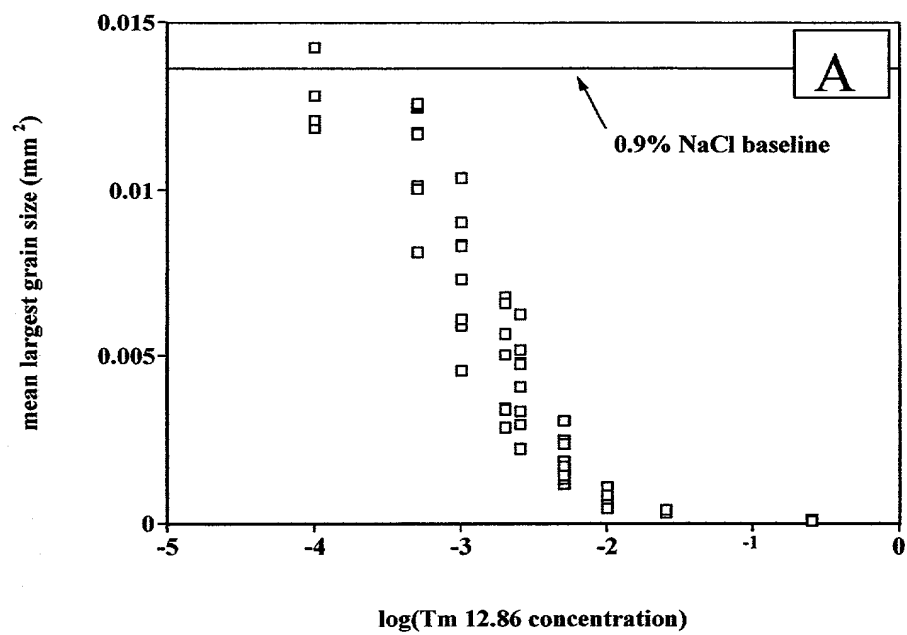


Fig. 8.16

2025-09-29 09:29:29

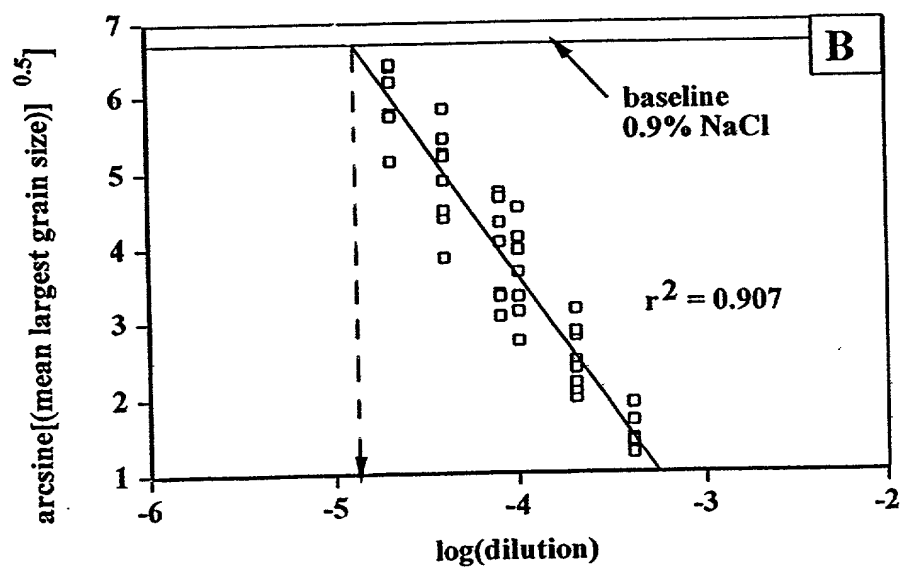
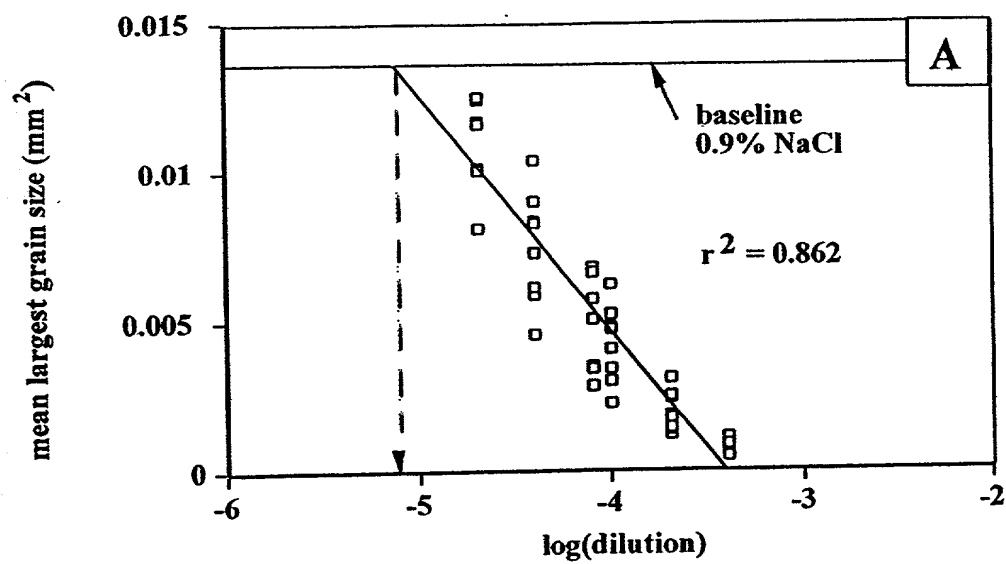


Fig. 8.17

2025 06 26 09:00

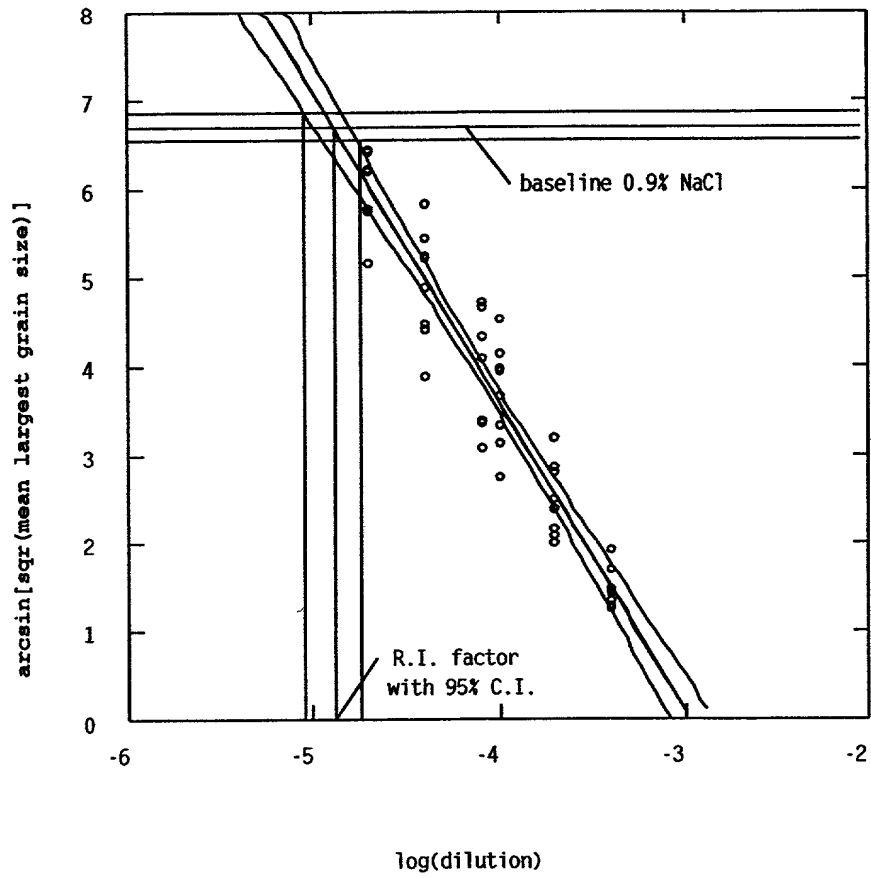


Fig. 8.18

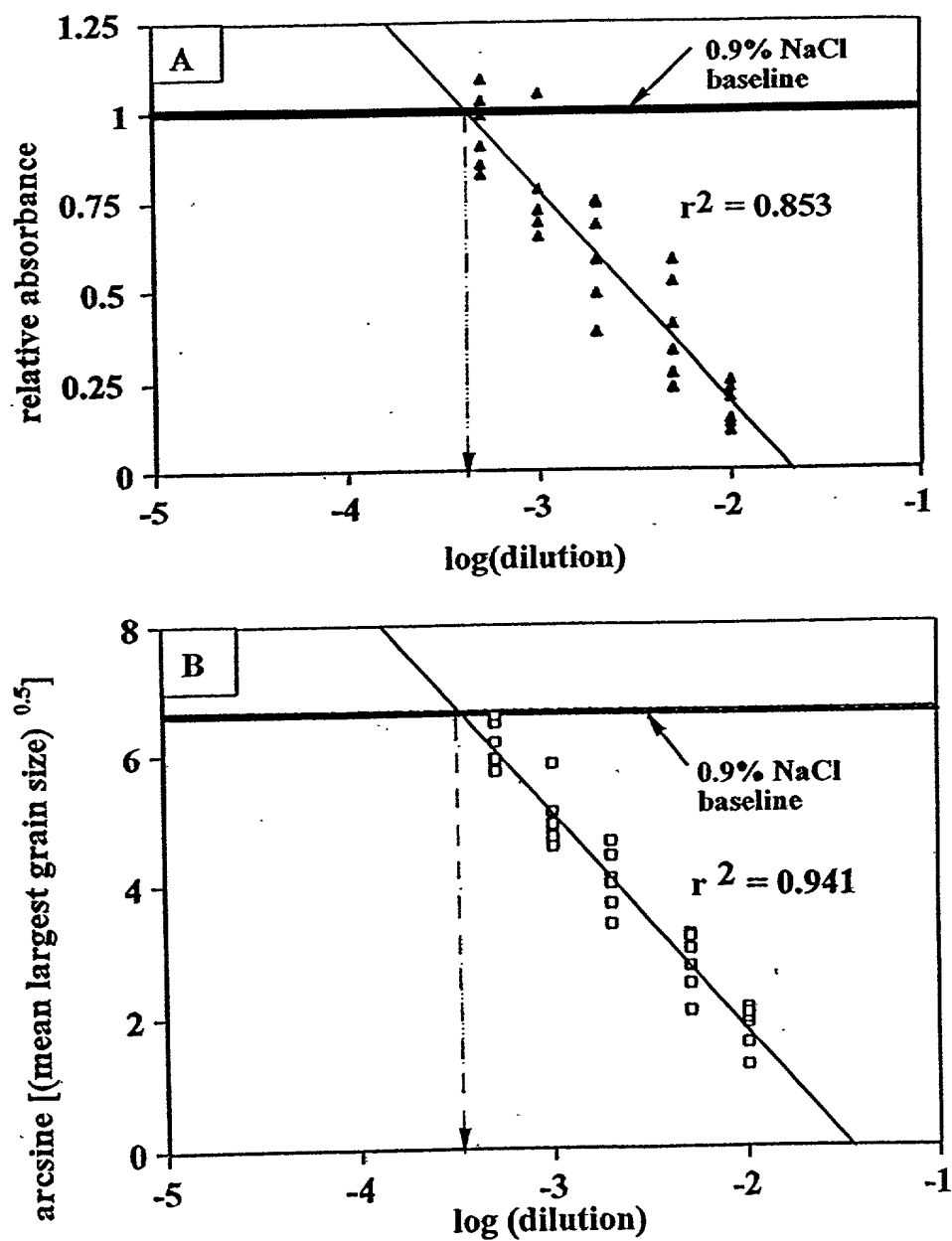


Fig. 8.19

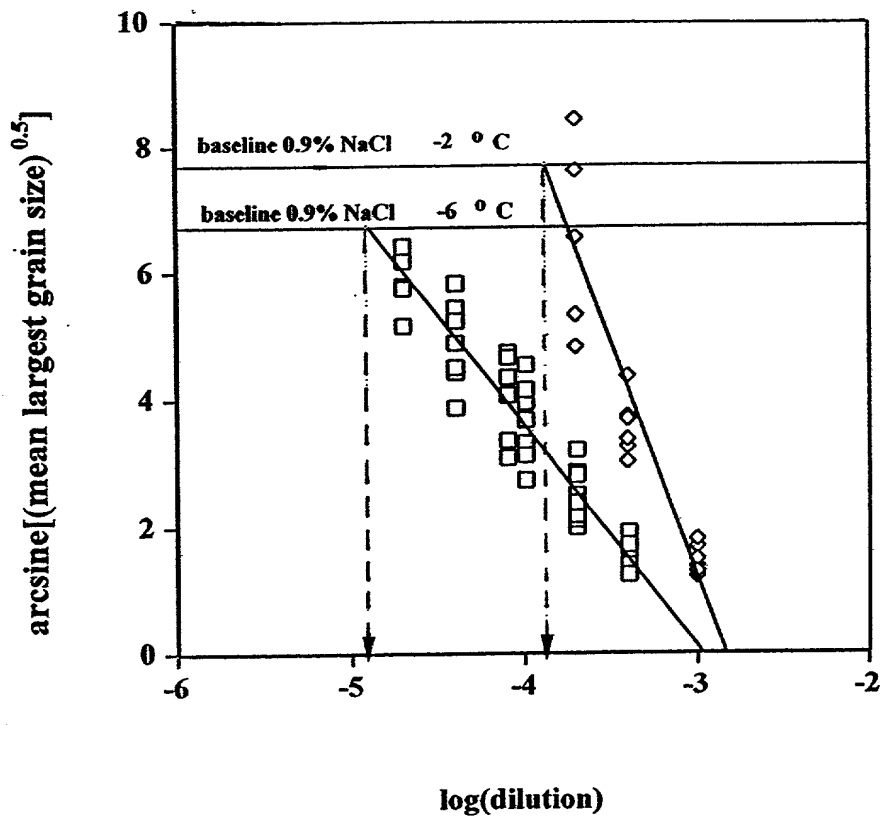


Fig. 8.20

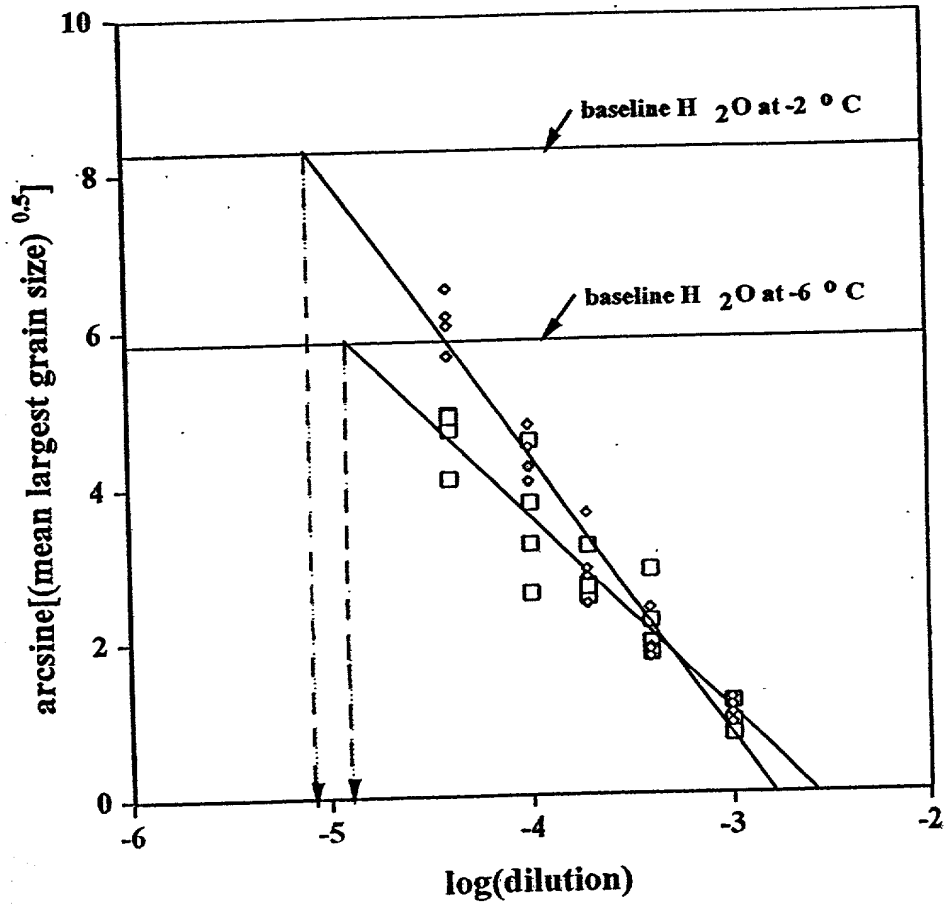


Fig. 8.21

20250306 09:29:00

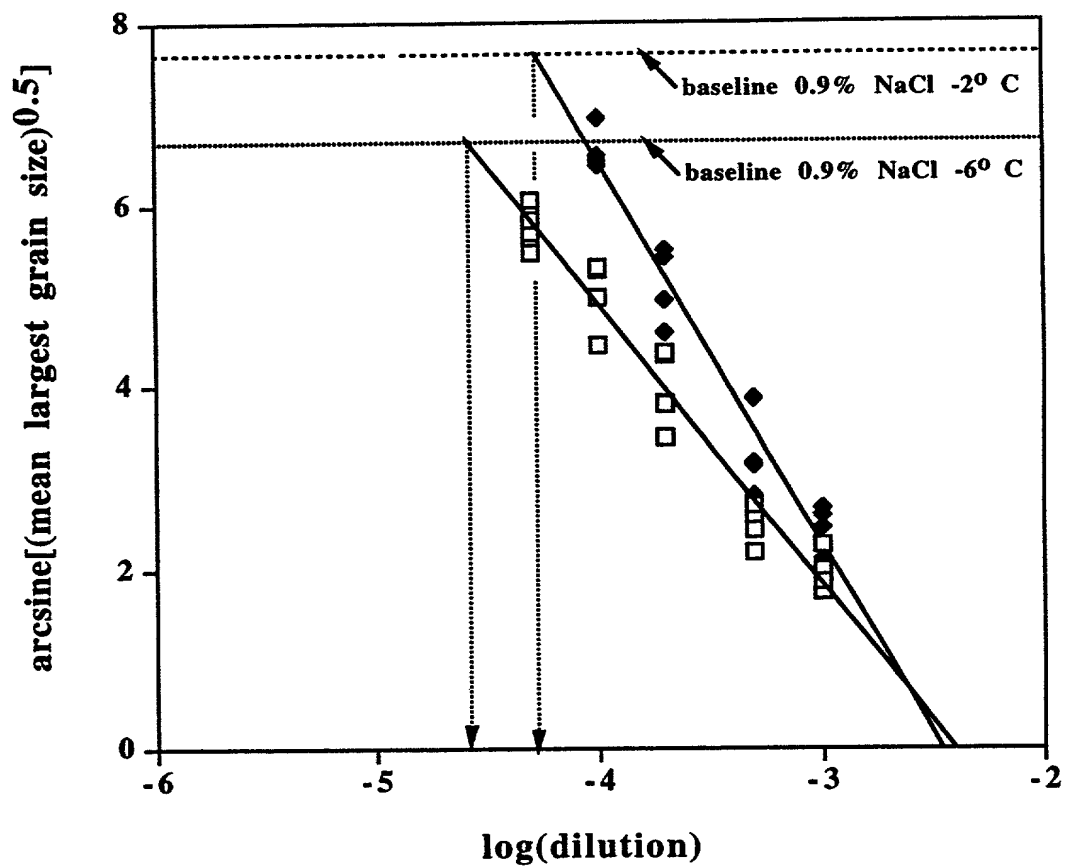


Fig. 8.22

2025-06-20 09:20:00

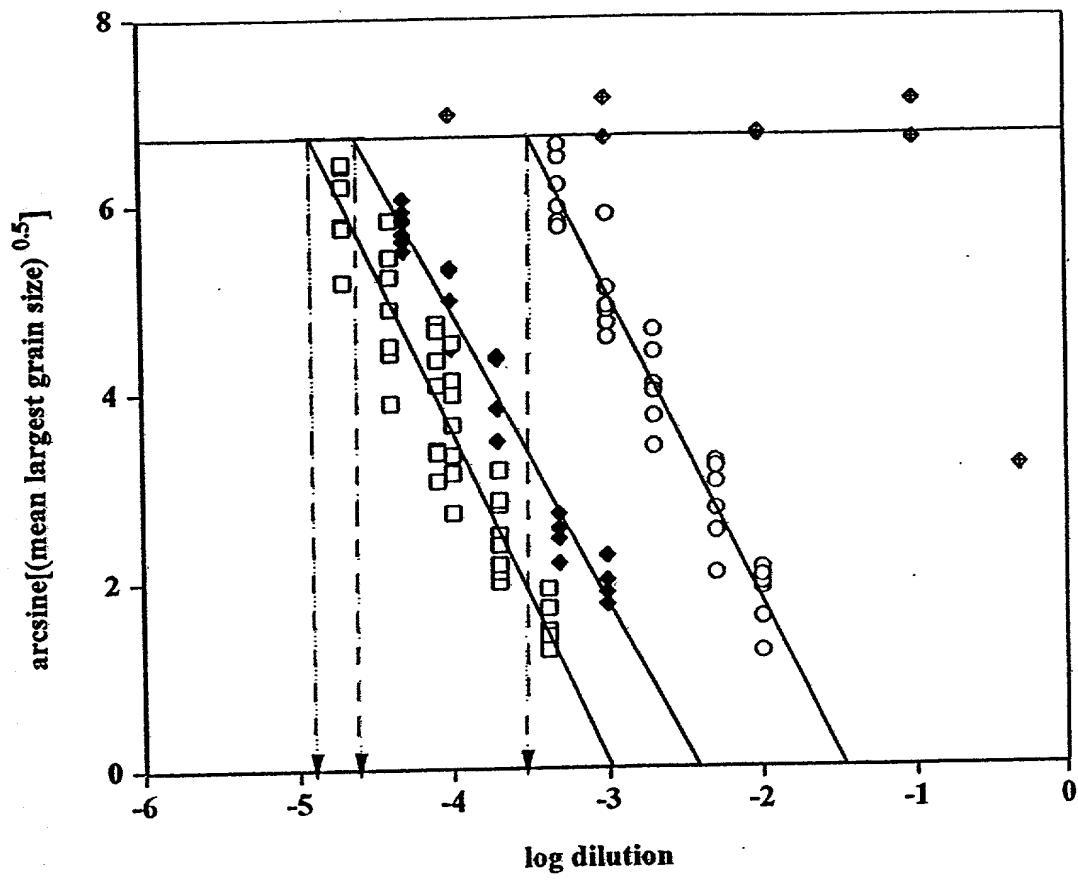


Fig. 8.23

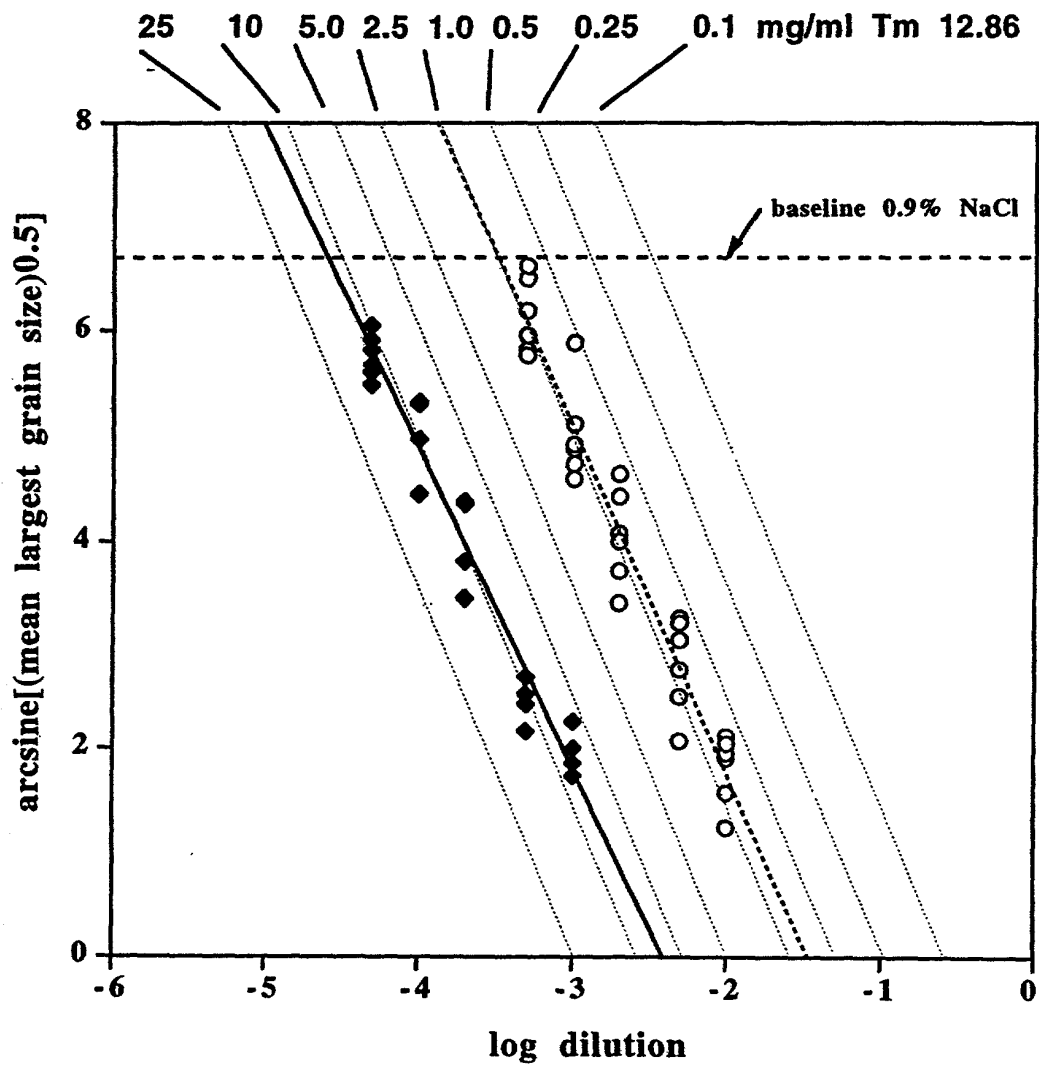


Fig. 8.24

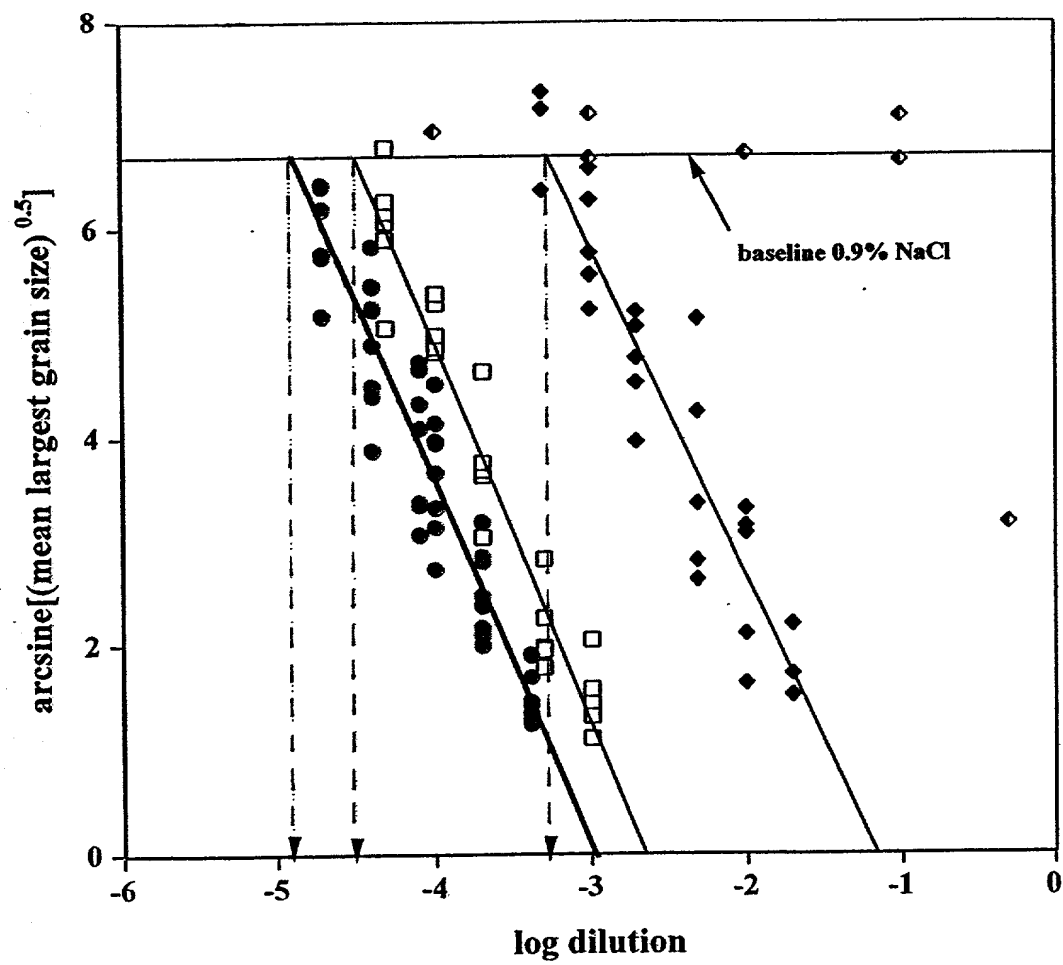


Fig. 8.25

202507 96292850

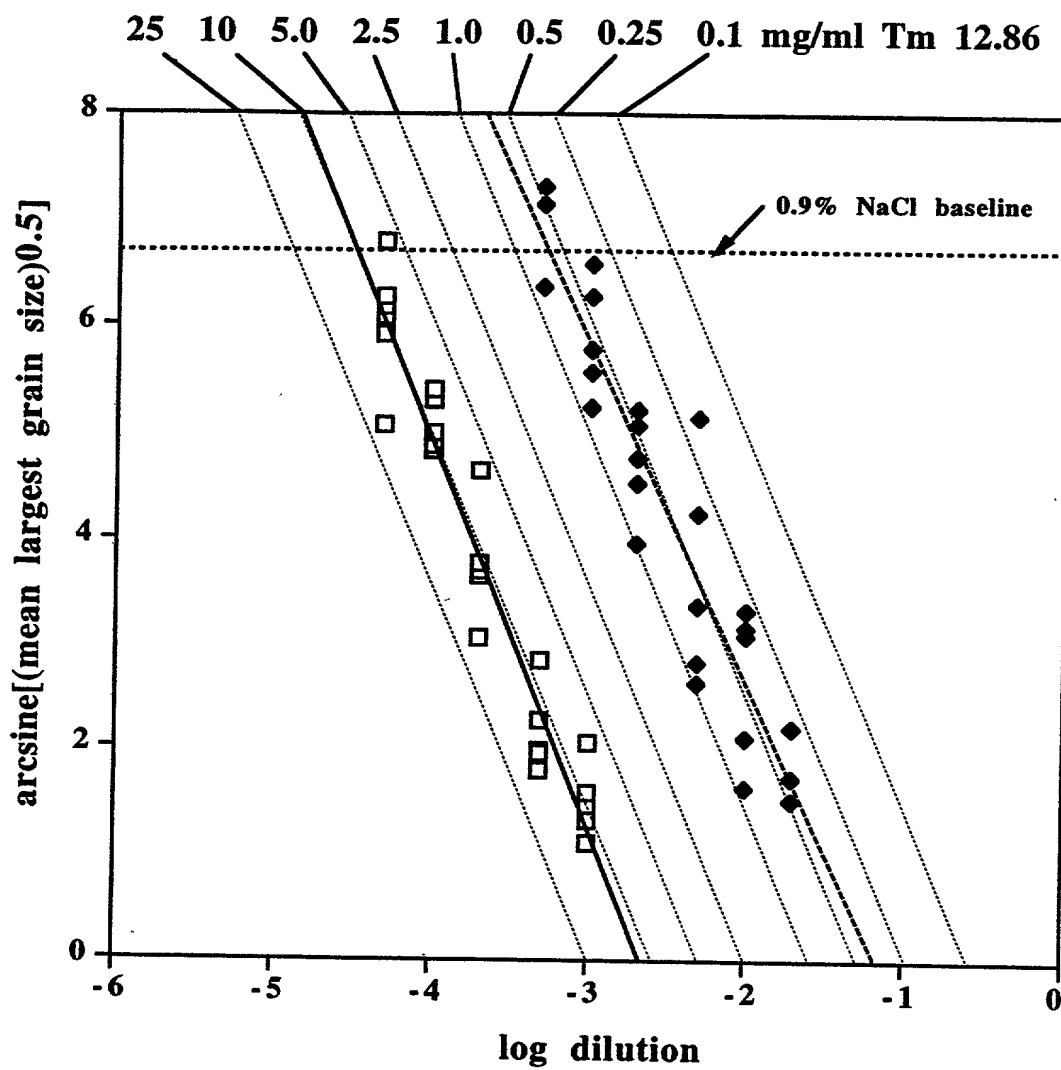


Fig. 8.26

2025-12-20 09:04:00

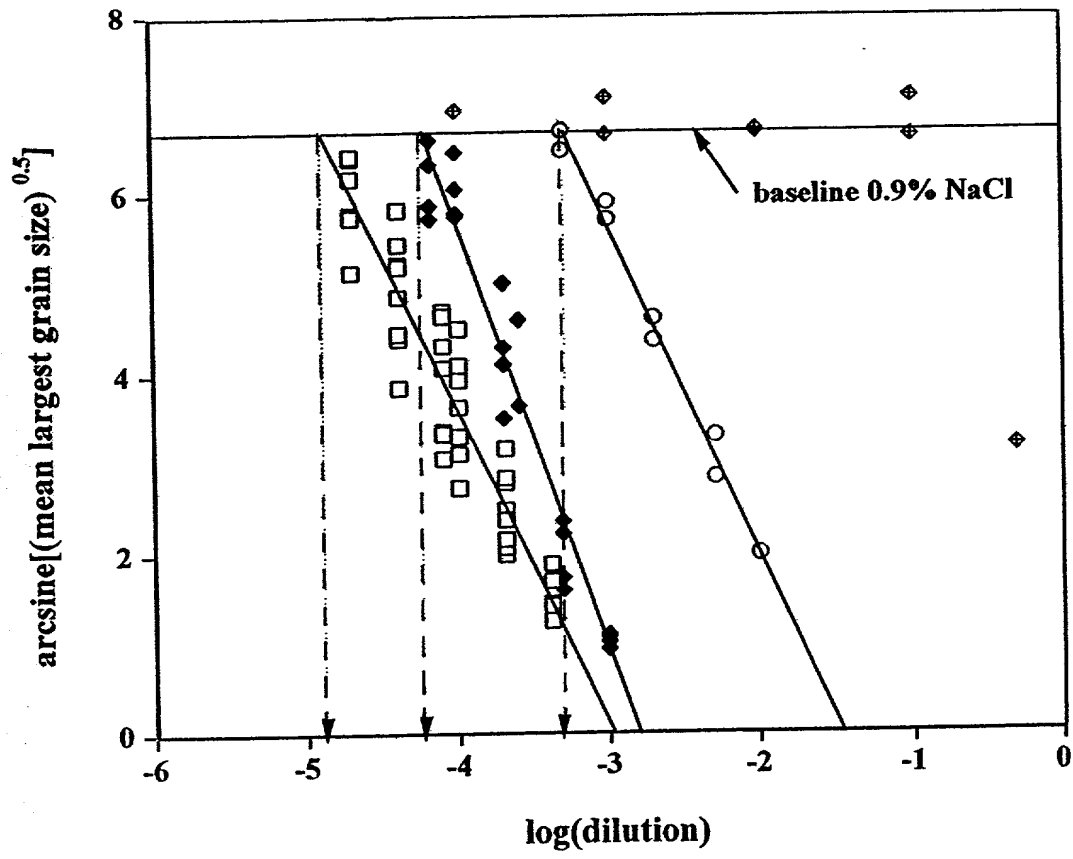


Fig. 8.27

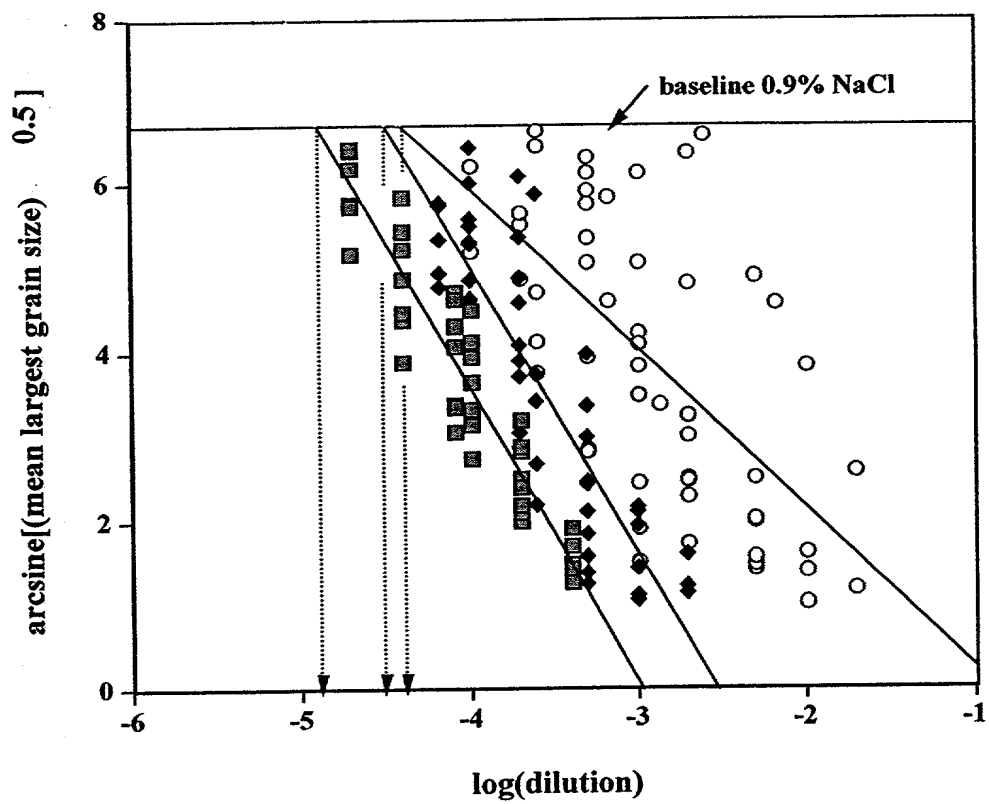


Fig. 8.28

$\arcsine[(\text{mean largest grain size})^{0.5}]$ 

Fig. 8.29

20250709 09:29:28

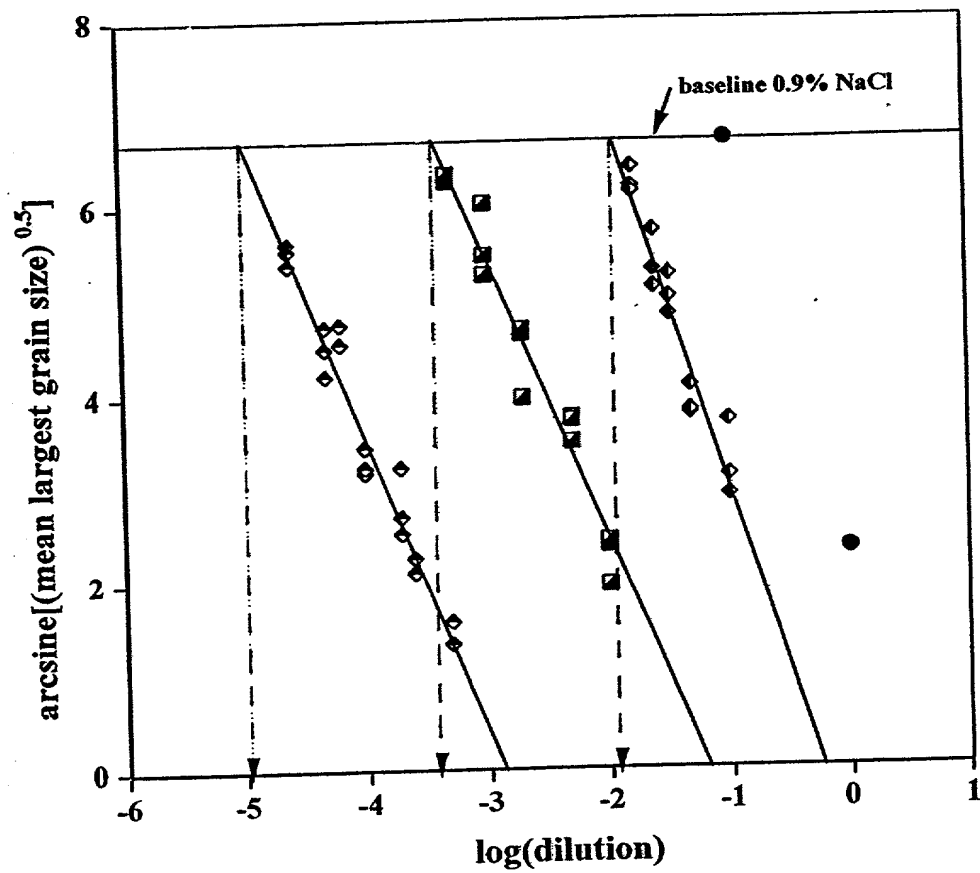


Fig. 8.30

2025-12-19 09:54:23

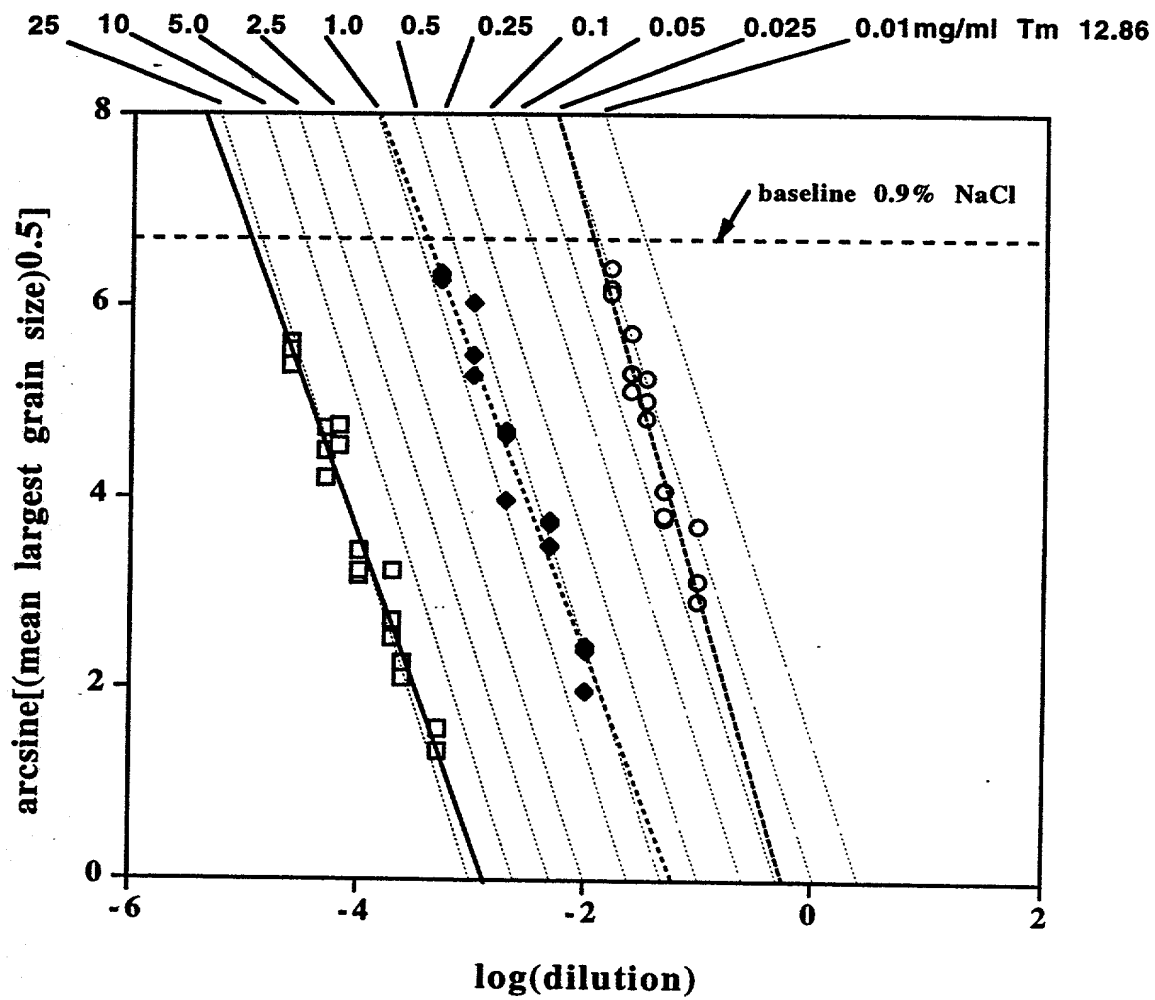


Fig. 8.31

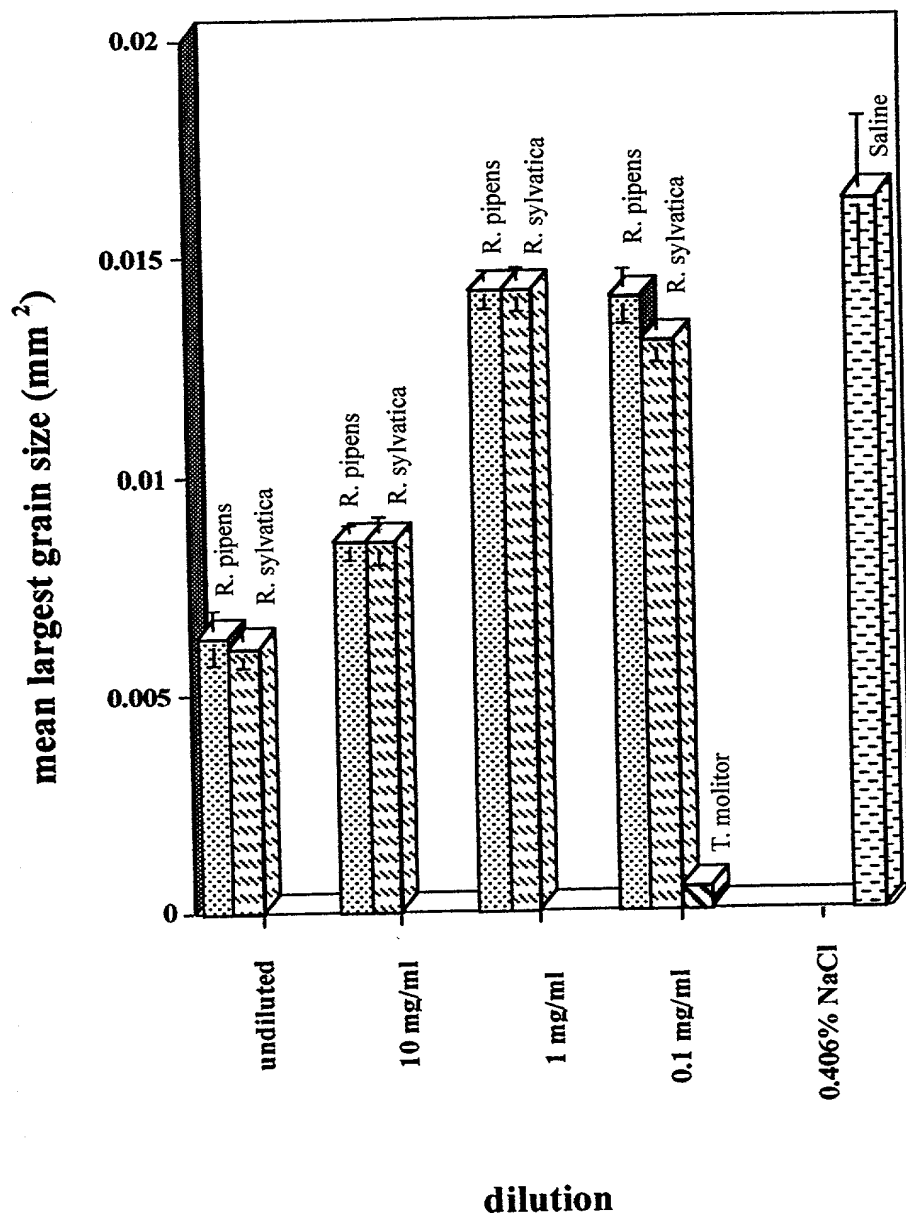


Fig. 8.32

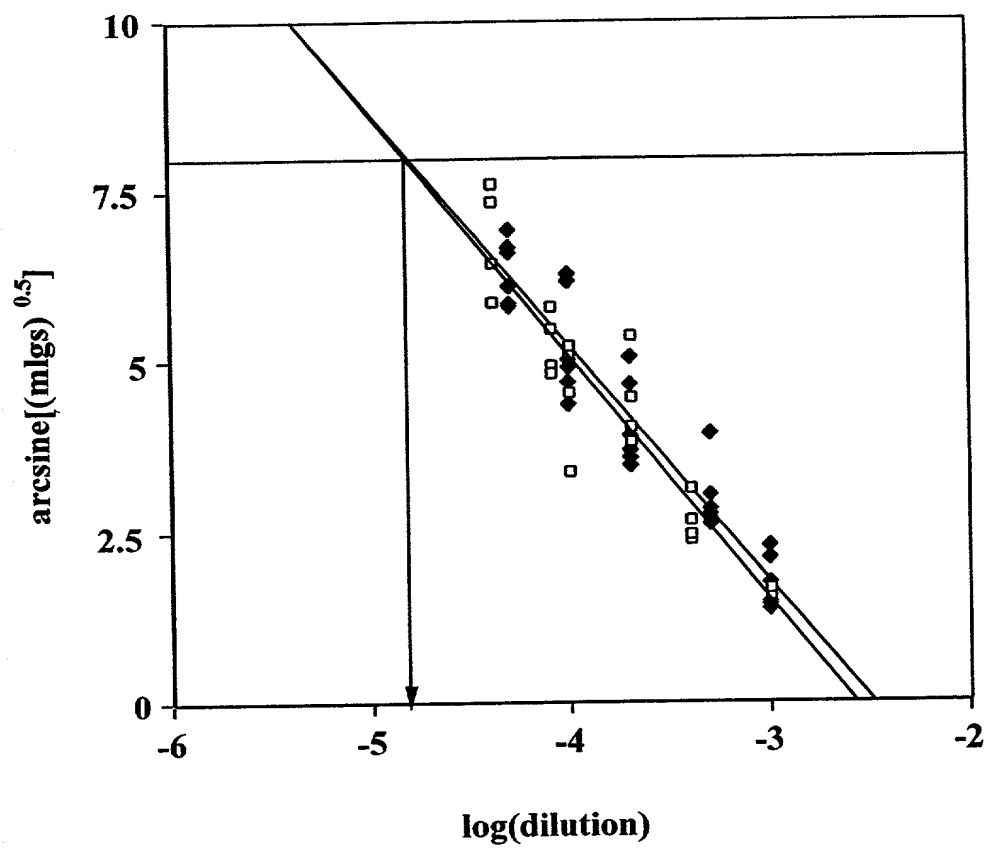


Fig. 8.33

2025-06-24 09:00

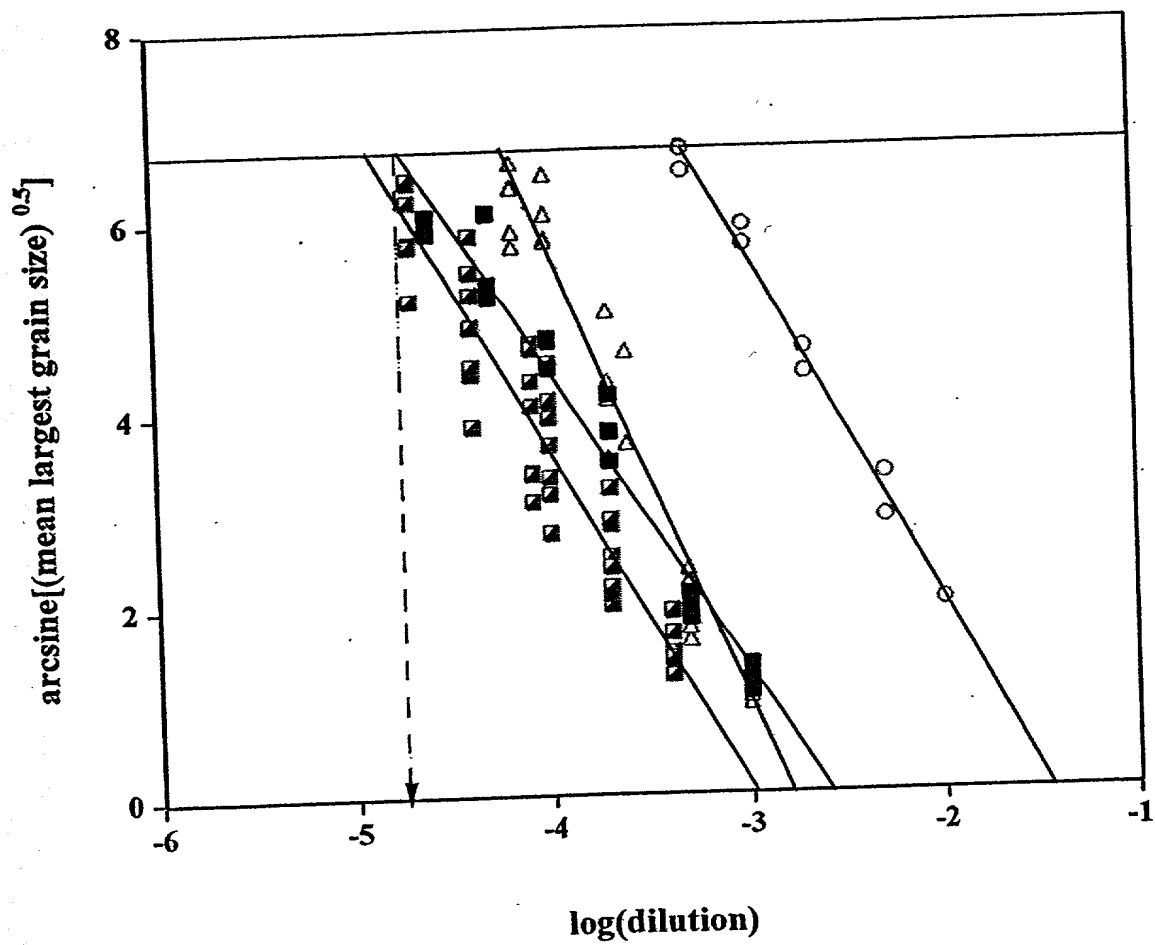


Fig. 8.34

20250624060

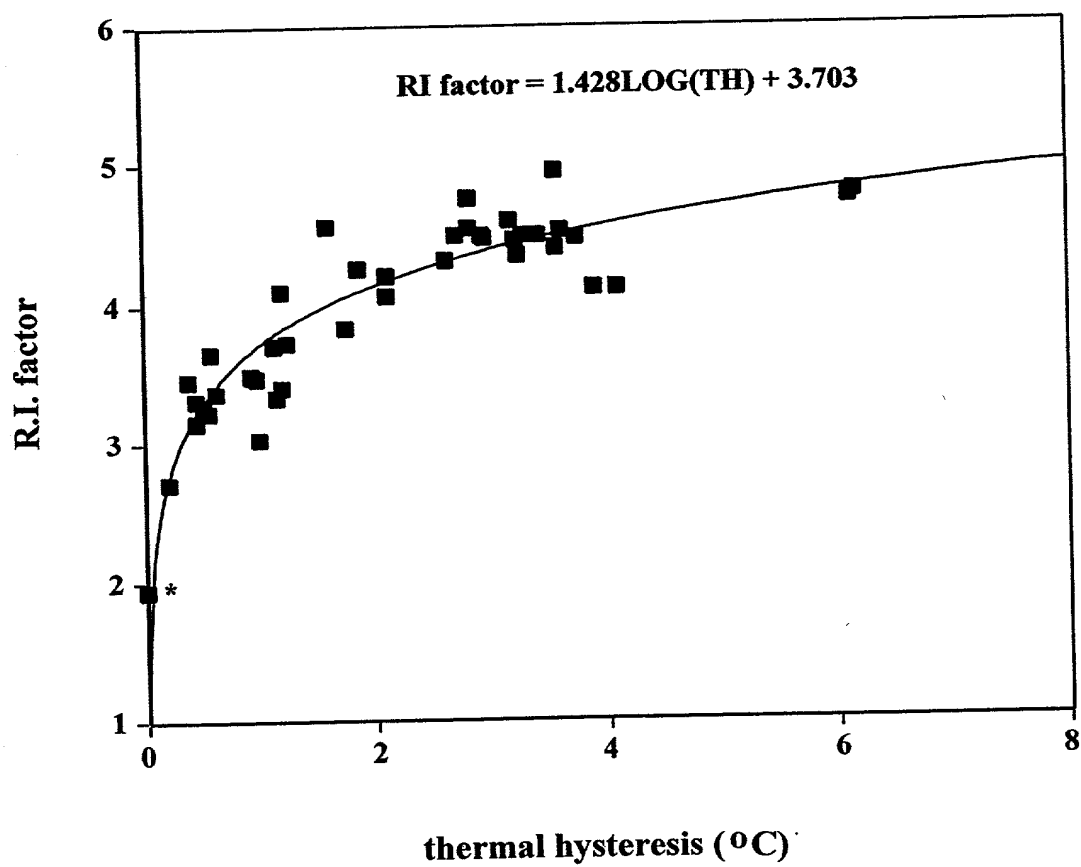


Fig. 8.35

2023-09-20 09:29:50

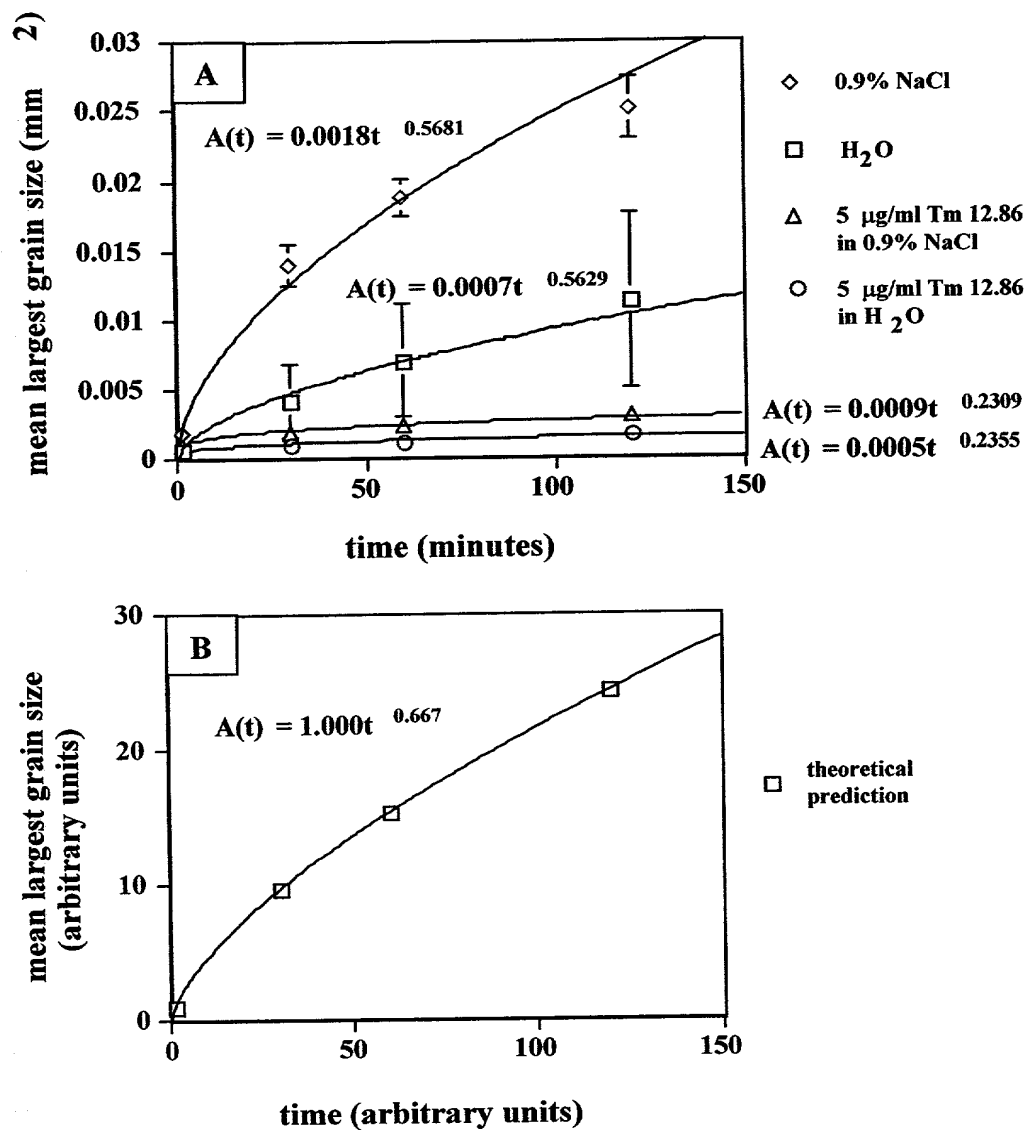


Fig. 8.36

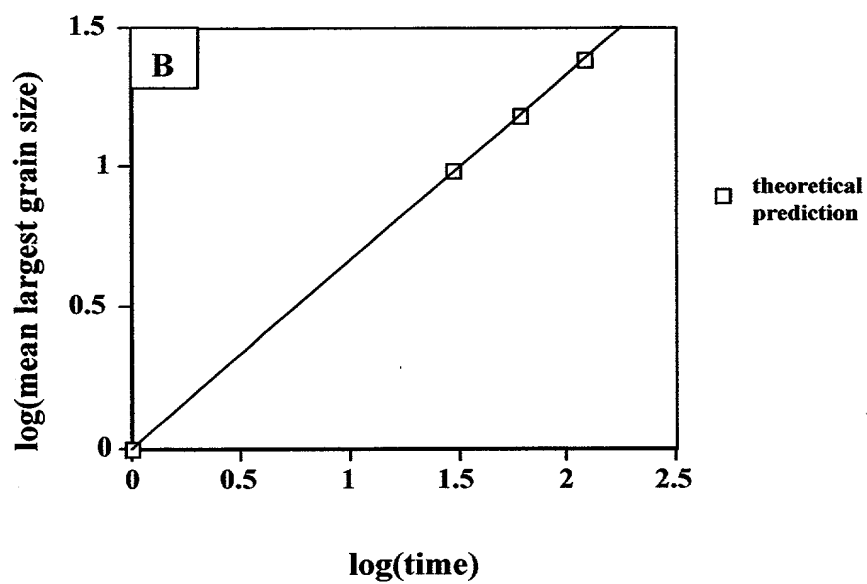
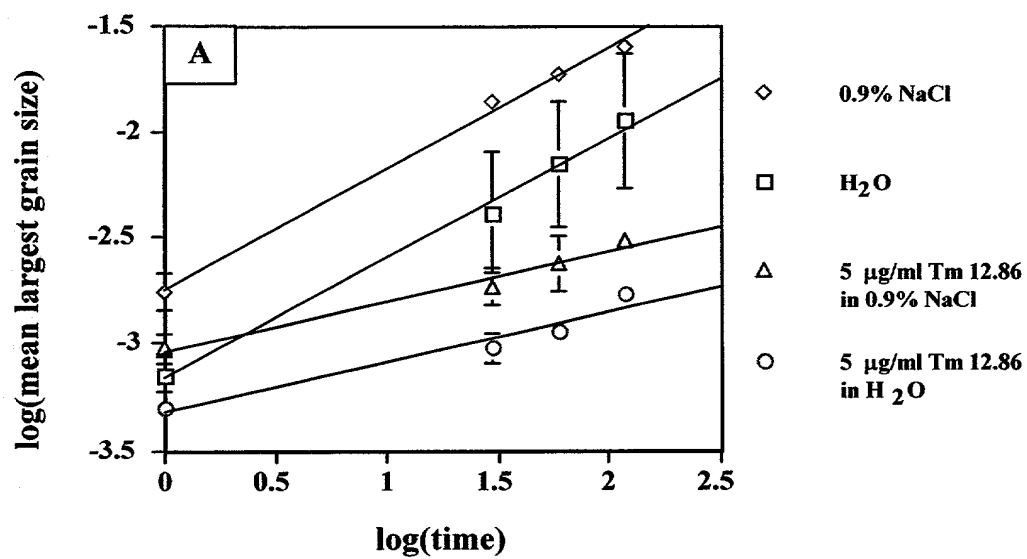
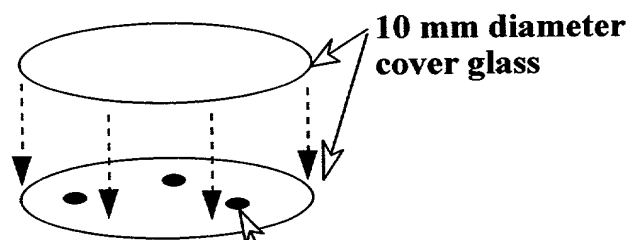


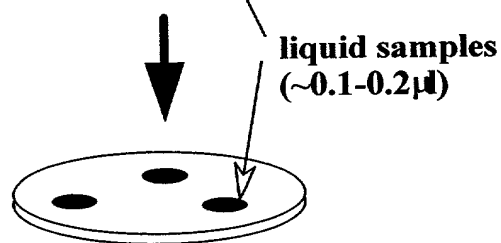
Fig. 8.37

"Sandwich" method of R.I. assessment

1.



2.



**3. FREEZE ON ~ -80 C
ALUMINUM PLATE (~ 10 MIN.)**



**4. PLACE ON COLD STAGE,
ANNEAL AT -6 C UP TO
12+ HOURS**

Fig. 8.38

Fig. 8.39

A circular, textured object, possibly a piece of fabric or a small globe, is centered against a black background. The object has a fine, grid-like texture. Five points are labeled with lowercase letters: 'a' is at the top, 'b' is on the right side, 'c' is at the bottom right, 'd' is at the bottom left, and 'e' is on the left side. A small white horizontal line is visible in the bottom right corner of the image.

Fig. 8.40

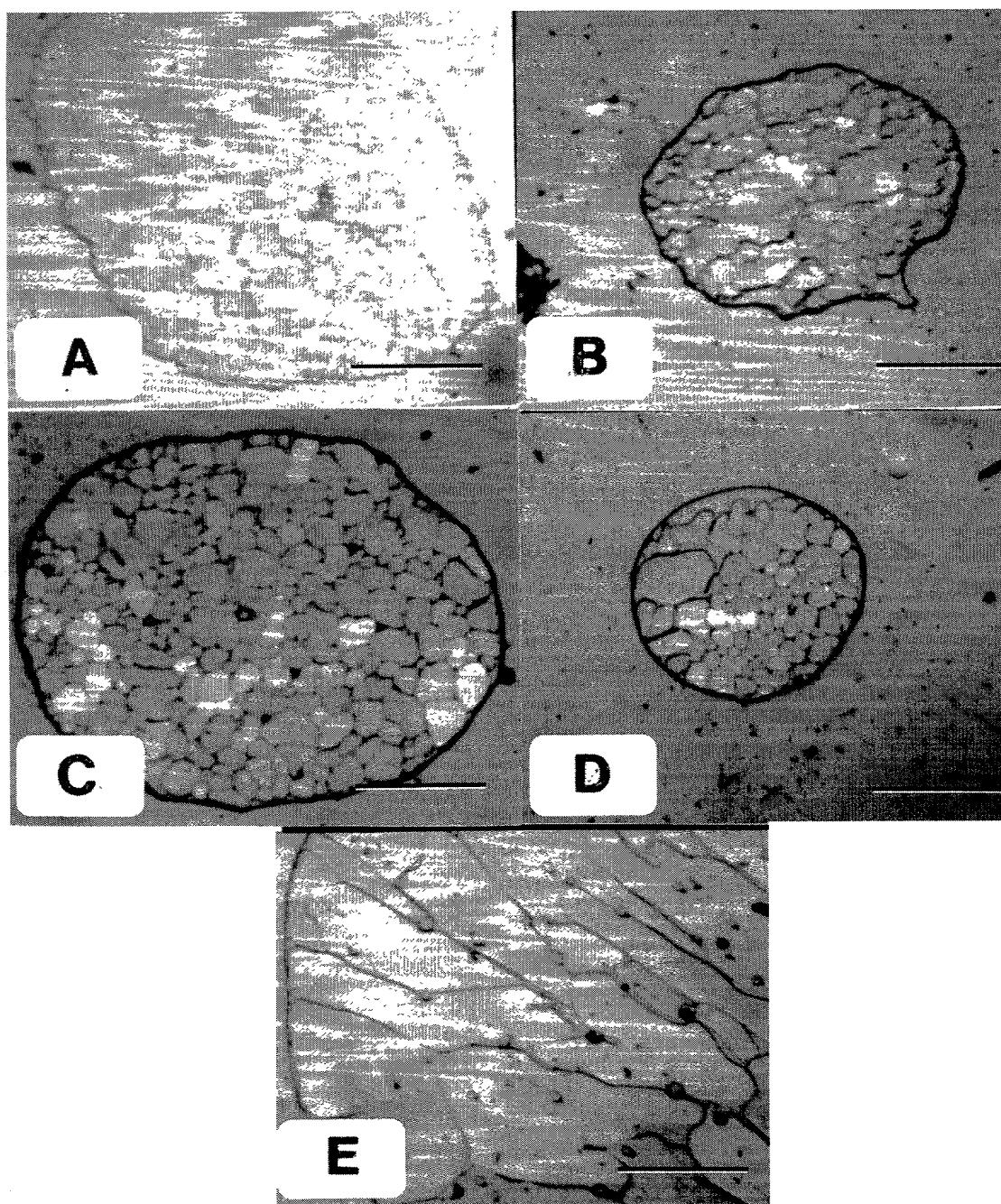


Fig. 8.41

090729Z 0200

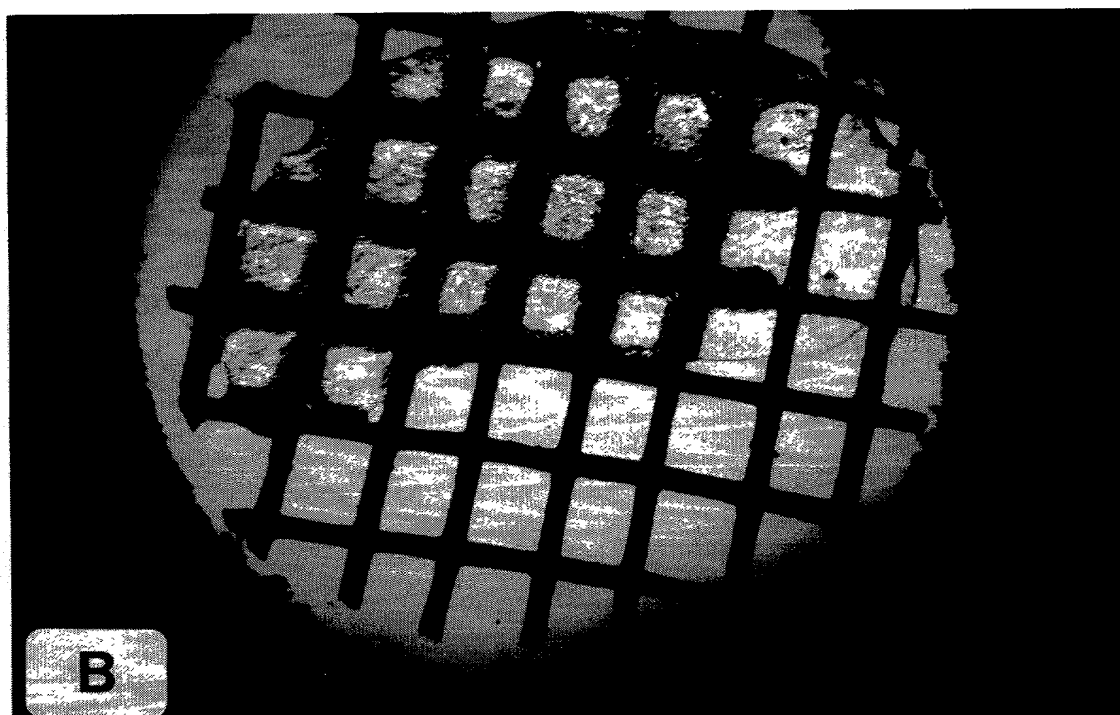
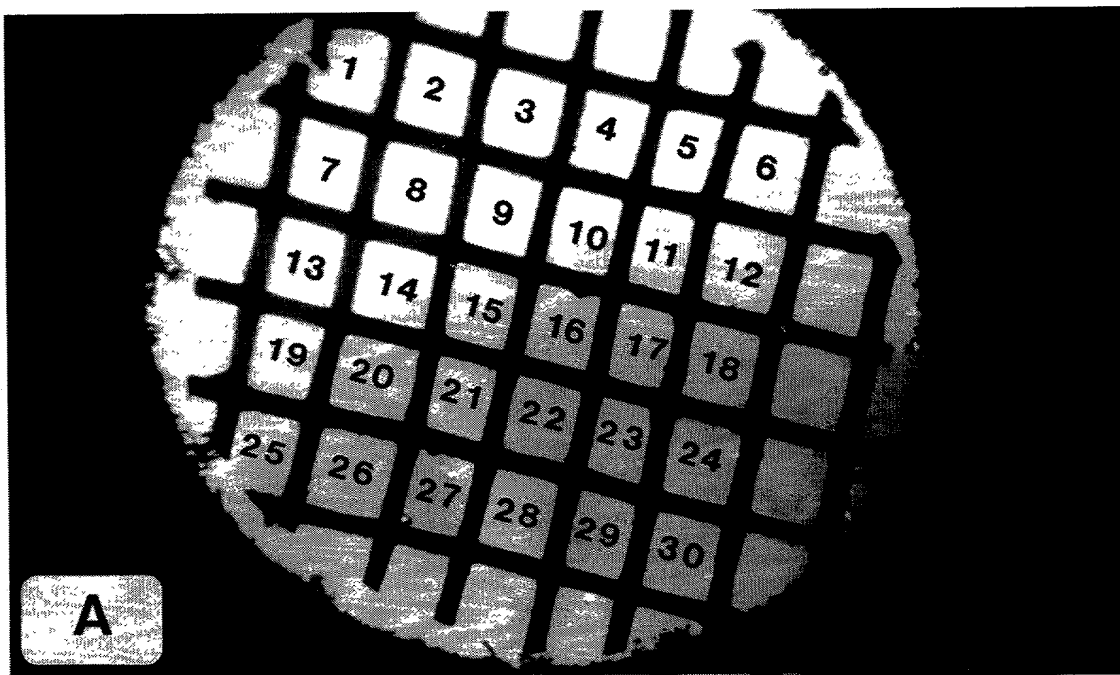


Fig. 8.42

DNA sequence of Tm 13.17 cDNA clone

B E
 a c
 m o
 H R
 I I

1 AGTGGATCCAAAGAATTCGGGCACGAGACTACTAAGATCAAGTTGCTCTGTTGTCTAATCT
 M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
 L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
 I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTGCGTGGCCAGGA
 N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAAGGTGA
 A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAAATCATCAATAAGTGCGCCGTCGAAGA
 K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTGTCATGAAAAACAAGCCAA
 D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
 F S P V D *

481 ATATAAAATAAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAAAAAACTCG
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTTCCACCC

X
 h
 o
 I

Fig. 8.43

09675796-604400

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTCCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

polyadenylation signal

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAA

poly (A) tail

Fig. 8.44